GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 02:15:49 ; Search time 218.096 Seconds
                                     (without alignments)
                                     246.943 Million cell updates/sec

Title: US-09-607-745-9
Perfect score: 1600
Sequence: 1 MDSKGSSQKSRLLLLLVVSN.........LNWIYNVWKAELSRHHHHHH 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1266	79.1	406	9	US-09-851-588-6	Sequence 6, Appli
2	1266	79.1	423	11	US-09-776-191-72	Sequence 72, Appl
3	1266	79.1	423	15	US-10-264-820-23	Sequence 23, Appl
4	1266	79.1	423	15	US-10-254-289-2	Sequence 2, Appli
5	1266	79.1	432	11	US-09-888-257A-7	Sequence 7, Appli
6	1266	79.1	432	11	US-09-946-374-275	Sequence 275, App
7	1266	79.1	432	12	US-10-015-387A-275	Sequence 275, App
8	1266	79.1	432	12	US-10-063-735-112	Sequence 112, App
9	1266	79.1	432	12	US-10-006-130A-275	Sequence 275, App
10	1266	79.1	432	12	US-10-106-172A-275	Sequence 275, App
11	1266	79.1	432	12	US-10-199-672-330	Sequence 330, App
12	1266	79.1	432	12	US-10-187-749-330	Sequence 330, App
13	1266	79.1	432	12	US-10-194-457-330	Sequence 330, App
14	1266	79.1	432	12	US-10-184-642-330	Sequence 330, App
15	1266	79.1	432	12	US-10-196-747-330	Sequence 330, App
16	1266	79.1	432	12	US-10-015-392A-275	Sequence 275, App
17	1266	79.1	432	12	US-10-017-253A-275	Sequence 275, App
18	1266	79.1	432	12	US-10-173-689-330	Sequence 330, App
19	1266	79.1	432	12	US-10-173-690-330	Sequence 330, App
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42	1266	79.1	432	12	US-10-176-759-330	Sequence 330, App
43	1266	79.1	432	12	US-10-176-920-330	Sequence 330, App
44	1266	79.1	432	12	US-10-176-922-330	Sequence 330, App
45	1266	79.1	432	12	US-10-176-924-330	Sequence 330, App

ALIGNMENTS

RESULT 1
US-09-851-588-6
; Sequence 6, Application US/09851588
; Patent No. US2002004267A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-68829-1/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/851,588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-588-6

Query Match   79.1%;
Best Local Similarity   97.4%;   Score 1266; DB 9; Length 406;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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    293 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 352

Qy  231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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Db  353 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 406
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RESULT 2
US-09-776-191-72
; Sequence 72, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-776-191-72

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Query Match             79.1%;  Score 1266;  DB 11;  Length 423;
Best Local Similarity   97.4%;  Pred. No. 6.2e-117;
Matches  228;  Conservative   2;  Mismatches   4;  Indels   0;  Gaps   0;

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Db  370 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 423
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RESULT 3
US-10-264-820-23
; Sequence 23, Application US/10264820
; Publication No. US20030108926A1
; GENERAL INFORMATION:
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030108926A1e1 Methods of Diagnosing Colorectal Cancer,
; TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
; TITLE OF INVENTION: Cancer Modulators
; FILE REFERENCE: 018501-006141US
; CURRENT APPLICATION NUMBER: US/10/264,820

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/268,866
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 09/435,945
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/436,983
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/450,857
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: US 09/453,850
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human CGA8
US-10-264-820-23

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Query Match             79.1%;  Score 1266;  DB 15;  Length 423;
Best Local Similarity   97.4%;  Pred. No. 6.2e-117;
Matches  228;  Conservative   2;  Mismatches   4;  Indels   0;  Gaps   0;

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Qy  111 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
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RESULT 4
US-10-254-289-2
; Sequence 2, Application US/10254289
; Publication No. US20030118509A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/10/254,289
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/656,002
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-254-289-2

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Query Match          79.1%;  Score 1266;  DB 15;  Length 423;
Best Local Similarity 97.4%;  Pred. No. 6.2e-117;
Matches 228;  Conservative  2;  Mismatches  4;  Indels  0;  Gaps  0;

Qy     51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Qy    231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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RESULT 5
US-09-888-257A-7

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;  Sequence 7, Application US/09888257A
;  Publication No. US20030060612A1
;  GENERAL INFORMATION:
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Hillan,Kenneth J.
;  APPLICANT:  Polakis,Paul
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Wu,Thomas D.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF TUMOR
;  FILE REFERENCE: P5002R1
;  CURRENT APPLICATION NUMBER: US/09/888,257A
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/063,540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: US 60/089,653
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: US 60/099,792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/103,678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: US 60/235,451
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: PCT/US99/20111
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US00/04342
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/06666
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 10
;  SEQ ID NO 7
;    LENGTH: 432
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;  TYPE: PRT
;  ORGANISM: Homo Sapien
US-09-888-257A-7

Query Match          79.1%;  Score 1266;  DB 11;  Length 432;
Best Local Similarity 97.4%;  Pred. No. 6.3e-117;
Matches 228;  Conservative  2;  Mismatches  4;  Indels  0;  Gaps  0;

Qy     51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Db    259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDELTPATP 318

Qy    171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
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Db    319 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy    231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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RESULT 6
US-09-946-374-275

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;  Sequence 275, Application US/09946374
;  Publication No. US2003007312A1
;  GENERAL INFORMATION:
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
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; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match   79.1%;   Score 1266; DB 11; Length 432;
Best Local Similarity 97.4%;   Pred. No. 6.3e-117;
  Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
           ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy 111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 319 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy 231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432

RESULT 7
US-10-015-387A-275
; Sequence 275, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2810P1C54
;   CURRENT APPLICATION NUMBER: US/10/015,387A
;   CURRENT FILING DATE: 2001-12-12
;   Prior Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-015-387A-275

Query Match   79.1%;   Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%;   Pred. No. 6.3e-117;
  Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
           ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy 111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 319 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy 231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432

RESULT 8
US-10-063-735-112
; Sequence 112, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P2330R1C1
;   CURRENT APPLICATION NUMBER: US/10/063,735
;   CURRENT FILING DATE: 2002-05-08
;   Prior Application removed - See Palm or File Wrapper
;   NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 112
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-735-112

Query Match   79.1%;   Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%;   Pred. No. 6.3e-117;
  Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
           ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 199 RVVGGEEASVDSWPWQVSIQYDKQHVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy 111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 319 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy 231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432

RESULT 9
US-10-006-130A-275
; Sequence 275, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-130A-275

  Query Match         79.1%;      Score 1266;  DB 12;  Length 432;
  Best Local Similarity   97.4%;  Pred. No. 6.3e-117;
  Matches 228;  Conservative  2;  Mismatches 4;  Indels  0;  Gaps  0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
            ::||| ||||||||||||||||||||||||||||||||||||||||||||
Db  199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy  111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy  171 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db  319 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy  231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
            |||||||||||||||||||||||||||||||||||||||||||
Db  379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
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RESULT 10
US-10-199-672-330
; Sequence 330, Application US/10199672
; Publication No. US2003014842A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-330

  Query Match         79.1%;      Score 1266;  DB 12;  Length 432;
  Best Local Similarity   97.4%;  Pred. No. 6.3e-117;
  Matches 228;  Conservative  2;  Mismatches 4;  Indels  0;  Gaps  0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
            ::||| ||||||||||||||||||||||||||||||||||||||||||||
Db  199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy  111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy  171 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db  319 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy  231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
            |||||||||||||||||||||||||||||||||||||||||||
Db  379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
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RESULT 11
US-10-006-172A-275
; Sequence 275, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
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PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
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PRIOR FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
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; PRIOR APPLICATION NUMBER: 60/105807
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; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match   79.1%;   Score 1266; DB 12; Length 432;
Best Local Similarity   97.4%;   Pred. No. 6.3e-117;
Matches 228;   Conservative   2;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Db   199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

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Db   259 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy   171 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
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Db   319 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 378

Qy   231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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Db   379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432

RESULT 12
US-10-187-749-330
; Sequence 330, Application US2003015036A1
; Publication No. US20030150368A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-330

Query Match   79.1%;   Score 1266; DB 12; Length 432;
Best Local Similarity   97.4%;   Pred. No. 6.3e-117;
Matches 228;   Conservative   2;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Qy   111 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
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Qy   171 LWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
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Qy   231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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Db   379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432

RESULT 13
US-10-194-457-330
; Sequence 330, Application US/10194457
; Publication No. US2003015037A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28

; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-330

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Query Match            79.1%;   Score 1266;  DB 12;   Length 432;
Best Local Similarity   97.4%;   Pred. No. 6.3e-117;
Matches 228;  Conservative   2;  Mismatches   4;   Indels   0;   Gaps   0;

Qy    51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Qy   111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
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Db   259 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318

Qy   171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
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Qy   231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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Db   379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
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RESULT 14
US-10-184-642-330
; Sequence 330, Application US/10184642
; Publication No. US2003015763A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C194
; CURRENT APPLICATION NUMBER: US/10/184,642
; CURRENT FILING DATE: 2002-06-27
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-642-330

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Query Match            79.1%;   Score 1266;  DB 12;   Length 432;
Best Local Similarity   97.4%;   Pred. No. 6.3e-117;
Matches 228;  Conservative   2;  Mismatches   4;   Indels   0;   Gaps   0;

Qy    51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Db   199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy   111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-330

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Db   379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
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RESULT 15
US-10-196-747-330
; Sequence 330, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C346
; CURRENT APPLICATION NUMBER: US/10/196,747
; CURRENT FILING DATE: 2002-07-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-747-330

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Query Match            79.1%;   Score 1266;  DB 12;   Length 432;
Best Local Similarity   97.4%;   Pred. No. 6.3e-117;
Matches 228;  Conservative   2;  Mismatches   4;   Indels   0;   Gaps   0;

Qy    51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Db   199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 258

Qy   111 KLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
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Qy   171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
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Qy   231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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Db   379 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
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Search completed: December 2, 2003, 02:51:18
Job time : 218.096 secs

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            GenCore version 5.1.6
    Copyright (c) 1993 - 2003 Compugen Ltd.

CM protein - protein search, using sw model

Run on:  December 2, 2003, 00:14:04 ; Search time 21.2875 Seconds
                                       (without alignments)
                                       580.377 Million cell updates/sec

Title:           US-09-607-745-9
Perfect score:   1600
Sequence:        1 MDSKGSGSSQKSRLLLLLVVSN........LNWIYNVWKAELSRHHHHHH 292

Scoring table:   BLOSUM62
                 Gapop 10.0., Gapext 0.5

Searched:        328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:   328717

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :  Issued Patents AA:*
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        4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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        6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	1266	79.1	423	4	US-09-656-002-2	Sequence 2, Appli
2	1266	79.1	435	3	US-09-008-271A-6	Sequence 6, Appli
3	765	47.8	316	4	US-09-387-375-9	Sequence 63, Appl
4	754.5	47.2	315	4	US-09-386-653A-9	Sequence 44, Appl
5	746	46.6	328	4	US-09-386-642-11	Sequence 68, Appl
6	740.5	46.3	327	4	US-09-386-629-8	Sequence 4, Appli
7	672.5	42.0	289	4	US-09-386-642-14	Sequence 6, Appli
8	645	40.3	288	4	US-09-386-642-13	Sequence 7, Appli
9	601.5	37.6	306	4	US-09-386-642-53	Sequence 2, Appli
10	593	37.1	319	4	US-09-386-642-12	Sequence 3, Appli
11	574	35.9	284	4	US-09-386-642-54	Sequence 2, Appli
12	526.5	32.9	418	1	US-08-508-448C-25	Sequence 4, Appli
13	526.5	32.9	418	4	US-09-370-838-82	Sequence 2, Appli
14	526.5	32.9	418	4	US-09-370-838-83	Sequence 13, Appl
15	524.5	32.8	418	4	US-09-370-838-62	Sequence 7, Appli
16	522.5	32.7	232	1	US-08-508-448C-19	Sequence 1, Appli
17	507	31.7	454	3	US-09-518-046-2	Sequence 1, Appli
18	506	31.6	492	4	US-09-342-749-2	Sequence 1, Appli
19	506	31.6	492	4	US-09-691-840-2	Sequence 2, Appli
20	505.5	31.6	376	4	US-09-820-002-2	Sequence 2, Appli
21	505.5	31.6	417	4	US-09-820-002-4	Sequence 4, Appli
22	499.5	31.2	256	4	US-09-027-337-3	Sequence 3, Appli
23	499.5	31.2	256	4	US-09-644-600-3	Sequence 3, Appli
24	497.5	31.1	255	3	US-08-944-483-67	Sequence 67, Appl
25	497	31.1	283	4	US-08-807-151-1	Sequence 1, Appli
26	497	31.1	283	4	US-09-478-957-1	Sequence 1, Appli
27	491.5	30.7	416	2	US-09-000-846-2	Sequence 2, Appli
28	489	30.6	638	2	US-08-681-151-3	Sequence 3, Appli
29	482	30.1	285	4	US-09-023-942A-26	Sequence 26, Appl
30	477	29.8	248	3	US-08-944-483-63	Sequence 63, Appl
31	463.5	29.0	246	3	US-08-978-404B-44	Sequence 44, Appl
32	463.5	29.0	250	3	US-08-944-483-68	Sequence 68, Appl
33	461.5	28.8	407	4	US-09-734-675-4	Sequence 4, Appli
34	456.5	28.5	314	4	US-09-023-942A-6	Sequence 6, Appli
35	455	28.4	284	4	US-09-387-375-7	Sequence 7, Appli
36	453.5	28.3	247	2	US-08-956-267A-2	Sequence 2, Appli
37	451.5	28.2	314	3	US-09-008-271A-3	Sequence 3, Appli
38	450.5	28.2	312	4	US-09-023-942A-4	Sequence 4, Appli
39	444	27.8	855	2	US-09-027-337-2	Sequence 2, Appli
40	444	27.8	855	2	US-09-644-600-2	Sequence 2, Appli
41	443	27.7	790	4	US-08-991-761A-13	Sequence 13, Appl
42	442.5	27.7	290	4	US-09-386-653A-7	Sequence 7, Appli
43	441.5	27.6	812	1	US-08-248-629A-1	Sequence 1, Appli
44	441.5	27.6	812	1	US-08-451-932-1	Sequence 1, Appli
45	441.5	27.6	812	1	US-08-452-260-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-656-002-2
; Sequence 2, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
;    APPLICANT: Mack, David
;    APPLICANT: Gish, Kurt
;    APPLICANT: Wilson, Keith
;    TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
;    TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
;    FILE REFERENCE: A-69108/DJB/JJD/AMS
;    CURRENT APPLICATION NUMBER: US/09/656,002
;    CURRENT FILING DATE: 2000-09-06
;    PRIOR APPLICATION NUMBER: US 09/525,993
;    PRIOR FILING DATE: 2000-03-15
;    PRIOR APPLICATION NUMBER: US 09/493,444
;    PRIOR FILING DATE: 2000-01-28
;    PRIOR APPLICATION NUMBER: PCT/US 00/07044
;    PRIOR FILING DATE: 2000-03-15
;    NUMBER OF SEQ ID NOS: 3
;    SOFTWARE: PatentIn version 3.0
;    SEQ ID NO 2
;    LENGTH: 423
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-656-002-2

  Query Match          79.1%;  Score 1266;  DB 4;  Length 423;
  Best Local Similarity 97.4%;  Pred. No. 5.5e-128;
  Matches 228;  Conservative 2;  Mismatches 4;  Indels 0;  Gaps 0;

Qy   51 KIVGGYALDVDSWPMQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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Qy  111 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEBLTPATP 170
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Qy  171 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTC 230
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  310 LWIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTC 369

Qy  231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGPSTPGVYTKVSAYLNWIYNVWKAEL 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  370 QGDSGGPLMYQSDQWHVVGIVSWGYGCGPSTPGVYTKVSAYLNWIYNVWKAEL 423

RESULT 2
US-09-008-271A-6
```

; Sequence 6, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Yue, Henry
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Tang, Tom Y.
;   APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Dr.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/008,271A
;   FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: <Unknown>
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Mohan-Peterson, Sheela
;   REGISTRATION NUMBER: 41,201
;   REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 435 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: COLNNOT13
;   CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-008-271A-6

Query Match   79.1%; Score 1266; DB 3; Length 435;
Best Local Similarity 97.4%; Pred. No. 5.7e-128;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy   51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
          ::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 261

Qy   111 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   262 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 321

Qy   171 LWIIGWGFTKQNGGMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   322 LWIIGWGFTKQNGGMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC 381

Qy   231 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   382 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 435

RESULT 3
US-09-387-375-9
; Sequence 9, Application US/09387375

; Patent No. 6485957
; GENERAL INFORMATION:
;   APPLICANT: Darrow, Andrew
;   APPLICANT: Andrade-Gordon, Patricia
;   APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/09/387,375
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-09-387-375-9

Query Match   47.8%; Score 765; DB 4; Length 316;
Best Local Similarity 51.1%; Pred. No. 3.4e-74;
Matches 164; Conservative 38; Mismatches 85; Indels 34; Gaps 10;

Qy   1 MDSKGGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDKIVGGYALDV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db   1 MDSKGGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDKIVGGYALED 60

Qy   61 DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFP---- 116
          :||||:||||||||||::|||::||::|||||||||||||||||||||||::|||
Db   61 GEWPWQASIQHGAHVCGGSLIAPQWVLTAAHCFRRALPABYRVRLGALRLGSTSPRTL 120

Qy   117 SLAVAKIIIIEFNPMYPKD--NDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWI 173
          :|:.|::::||::::||:.|::|::||::||:|||::||:|||||||||||||||||||
Db   121 SVPVRRVLL--PPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRV 177

Qy   174 IGWGFTKQNGGKMSD-ILLQASVQVIDSTRCN----ADDAYQGE--VTEKMMCAGIPE 224
          |||:||||||||:||.:|::|:|||||:|:.|:|::|::|
Db   178 TGWG-SLRPGVPLPEWRPLQGVRPLLDSRTCDGLYHVGADVPQAERIVLPGSLCAGYPQ 236

Qy   225 GGVDTCQGDSGGPL-MYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI------ 276
          ||||:|||||||||.:|||||||||||||||||||||||||||||||||||:|:
Db   237 GHKDACQGDSGGPLTCLQSGSGSWVLVGVVSWGKGCALPNRPGVYTSVATYSPWIQARVTSN 296

Qy   277 -----YNVWKAELSRHHHHHH 292
                 |::|||||:|||||||
Db   297 ASRYPYDV-PDYAARHHHHHH 316

RESULT 4
US-09-386-653A-9
; Sequence 9, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
;   APPLICANT: Darrow, Andrew
;   APPLICANT: Andrade-Gordon, Patricia
;   APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 315
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
;   OTHER INFORMATION: of Protease T in a zymogen activation construct
US-09-386-653A-9

```
Query Match          47.2%;    Score 754.5;   DB 4;    Length 315;
Best Local Similarity  48.4%;    Pred. No. 4.6e-73;
Matches 156;  Conservative 46;  Mismatches 83;  Indels 37;  Gaps 10;

Qy    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDV 60
Db    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALEE 60

Qy   61 DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL--GSFPSLA 119
Db   61 GEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM 120

Qy  120 VAKIIIIEFNPNY---PKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPL--WII 174
Db  121 YARVRQVESNPHYQGTASSADVALVELEAPVPFTNYILPVCLP--DPSVIFBTGMNCWVT 178

Qy  175 GWGFTKQNGGKRMSD------ILLQASVQVIDSTRCN------ADDAYQGE-VTEKMMCAG 221
Db  179 GWGSPSE-----EDLLPEPRILQLAVPIIDTPKCNLLYSKDTBFGYQPKTIKNDMLCAG 233

Qy  222 IPEGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNV- 279
Db  234 FEEGKKDACKDSGGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII 293

Qy  280 ------WKAELSRHHHHHH 292
Db  294 PKLQFQPPARLGGQKSRHHHHHH 315
```

RESULT 5
US-09-386-642-11
; Sequence 11, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11

```
Query Match          46.6%;    Score 746;    DB 4;    Length 328;
Best Local Similarity  49.7%;    Pred. No. 4e-72;
Matches 163;  Conservative 35;  Mismatches 94;  Indels 36;  Gaps 8;

Qy    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDV 60
Db    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALEA 60

Qy   61 DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLA- 119
Db   61 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKRAYEVKLGAHQLDSYSEDAK 120

Qy  120 VAKIIIIEFNPMPKD--NDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGW 176
Db  121 VSTLKDIIPHPSILQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTVTGW 180

Qy  177 GFTKQNGGKMS-DILLQASVQVIDSTRCNA---DDAYQGE---VTEKMMCAGIPEGGVDT 229
Db  181 GHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDA 240
```

```
Qy  230 CQGDSGGPLMYQSD-QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIY------ 277
Db  241 CQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVVTLASSYASWIQSKVTELQPRVV 300

Qy  278 ------NVWKAEL--SRHHHHHH 292
Db  301 PQTQESQPDSNLCGSHLAFSSRHHHHHH 328
```

RESULT 6
US-09-386-629-8
; Sequence 8, Application US/09386629
; Patent No. 6426199
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L.
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Idenification and Characterization of the complementary
; TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
; FILE REFERENCE: ORT-1030
; CURRENT APPLICATION NUMBER: US/09/386,629
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
; OTHER INFORMATION: domain fusion protien
US-09-386-629-8

```
Query Match          46.3%;    Score 740.5;   DB 4;    Length 327;
Best Local Similarity  49.8%;    Pred. No. 1.6e-71;
Matches 164;  Conservative 39;  Mismatches 87;  Indels 39;  Gaps 10;

Qy    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDV 60
Db    1 MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALED 60

Qy   61 DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTD-VFNWKVRAGSDKLGSFPSLA 119
Db   61 SEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGN-PGSR 119

Qy  120 VAKIII--IEFNPMYP-KDN---DIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWI 173
Db  120 SQKVGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWI 179

Qy  174 IGWGFTKQNGGKM--SDILLQASVQVIDSTRCNA---DDAYQGEVTEKMMCAGIPEGGVD 228
Db  180 SGWG-SIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPPITEDMLCAGYLEGERD 238

Qy  229 TCQGDSGGPLMYQSD-QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWK----- 281
Db  239 ACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRG 298

Qy  282 ------AELSRHHHHHH 292
Db  299 RAQGGGALRAPSQGSGAAARSRHHHHHH 327
```

RESULT 7
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
;

```
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match             42.0%;  Score 672.5;  DB 4;  Pred. No. 2.8e-64;  Length 289;
Best Local Similarity   48.5%;
Matches  148;  Conservative  39;  Mismatches  89;  Indels  29;  Gaps  11;

Qy    1  MDSKGSSQKSRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDKIVGGY-ALD   59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db    1  MDSKGSSQKSRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDKIVGGYNCLE   60

Qy   60  VDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRK----HTDVFNWKVRAGSDK---  111
            ||||| :||   :|  ||||||| :::| ||||||  |
Db   61  KHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNLQKEEGCEQTRTA 120

Qy  112  LGSFPSLAVAKIIIEFNPMYP-KD--NDIALMKLQFPLTFSGTVRPICLPFFDEELTPA  168
            :||| :  ||  ::|: ||: ||   :|| ||| :   ||||||
Db  121  TESFPHPG-------FNNSLPNKDHRNDIMLVKMASPVSITWAVRPLITLS--SRCVTAG 170

Qy  169  TPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVD 228
            | :|| ||| ::   |:   :| :  ::|: |:|| | :||    : |:||| |||
Db  171  TSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKC--ENAYPGNITDTMVCASVQEGGKD 228

Qy  229  TCQGDSGGPLMYQSDQWHVVGIVSWGYG-CGGPSTPGVYTKVSAYLNWIYNVWKAELSRH 287
            ||||||||||:     ||| |::|||   || :| |||||| |  ::|| :   ||:||
Db  229  SCQGDSGGPLVCNQS---LQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN-SRH 284

Qy  288  HHHHH  292
            |||||
Db  285  HHHHH  289


RESULT 8
US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13

Query Match             40.3%;  Score 645;  DB 4;  Pred. No. 2.6e-61;  Length 288;
Best Local Similarity   47.9%;
Matches  146;  Conservative  38;  Mismatches  91;  Indels  30;  Gaps  11;
```

```
Db   61  PHSQPWQAALFQGGQQLLCGGVLVGGNWVLTAAHCKKPKYT-----VRLGDHSLQNKDGP 114
            ||||| :: :|||||  ||  ::  :|||||||    |
Qy  115  FPSLAVAKIIIEFNPMY------PKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPA  168
            :|||   :||      | :|  ||: :|||| |   ||||||||||||||||||||||
Db  115  EQBIPVVQSIP--HPCYNSSDVBDHNHDLMLLQLRDQASLGSKVKPISLA--DHCTQPG  169
Qy  169  TPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVD 228
            | :|| ||| |:   ||  :: :| :  :::| | |:    :|:|    :: |:||| |
Db  170  QKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKC--EDAYPGQITDGMVCAGSSK-GAD 226
Qy  229  TCQGDSGGPLMYQSDQWHVVGIVSWGYG-CGGPSTPGVYTKVSAYLNWIYNVWKAELSRH 287
            ||||||||||:     ||| ||:|||   ||  :  |||||: |  :||  :: ||:||
Db  227  TCQGDSGGPLVCDG---ALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSKGSRH 283
Qy  288  HHHHH  292
            |||||
Db  284  HHHHH  288


RESULT 9
US-09-386-642-53
; Sequence 53, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 53
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
; OTHER INFORMATION: human protease F in CFEK2 zymogen vector
US-09-386-642-53

Query Match             37.6%;  Score 601.5;  DB 4;  Length 306;
Best Local Similarity   42.9%;  Pred. No. 1.3e-56;
Matches  126;  Conservative  46;  Mismatches  85;  Indels  37;  Gaps  10;

Qy   28  VSDYKDDDDVDAAALAAPFDDDKIVGGYALDVSWPWQVSIQYDKQHVCGGSILDPHVV   87
            |||||||| ||||||||||||||||||| |  ||:|||  | :|  ||| :|||
Db   21  VPDYKDDD--DAAALAAPFDDDKIVGGYALELGRWPWQGSLRLWDSHVCGVSLLSHRWA   78
Qy   88  LTAAHCFRKHTDVFN--WKVRAGSDKLGSFPSLAVAK------IIIEFNPMYPKDN-  136
            |||||||  ::|:|   |:   |::   :: :|  :|      ||||||||||||:
Db   79  LTAAHCFETYSDLSDPSGWMVQFG--QLTSMPSFWSLQAYNRYFVSNIYLSPRYLGNSP 136
Qy  137  -DIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQ-AS 194
            ||||:||   :|| :|  :|| ||:  | |  | :|| ||| :|:   |:|||| :
Db  137  YDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGVYIKEDEALPSPHTLQEVQ 196
Qy  195  VQVIDSTRCN--ADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPL-MYQSDQWHVVGI  250
            | :: :: ||   |: ::  :   :|||| |:|| | |||||||||    |:| |:||
Db  197  VAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIGV  256
Qy  251  VSWGYGCGGPSTPGVYTKVSAYLNWIYNV-----------WKAELSRHHHHHH  292
            |||| || :| :|||||: |   ||| :|           ||||:|||||||
Db  257  VSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSW----SRHHHHHH  306


RESULT 10
US-09-386-642-12
; Sequence 12, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
```

```
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Zymogen Activation System
;  FILE REFERENCE: ORT-1028
;  CURRENT APPLICATION NUMBER: US/09/386,642
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
;
;  SEQ ID NO 12
;  LENGTH: 319
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;  OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-12

Query Match             37.1%;  Score 593;  DB 4;  Length 319;
Best Local Similarity   44.2%;  Pred. No. 1.2e-55;
Matches   133;  Conservative   35;  Mismatches   95;  Indels   38;  Gaps    9;

Qy          28  VSDYKDDDDVDAAALAAPFDDDDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWV  87
                   |||||||   ||||||||||||||||:||   :||  :||||:|  :||||||:
Db          21  VPDYKDDD--DAAALAAPFDDDDKIVGGYALEAGQWPWQVSITYEGVHVCGGSLVSEQWV  78

Qy          88  LTAAHCPRKHTDVFNWKVRAGSDKLGSFPSLA-VAKIIIEBNPMYPKD--NDIALMKL  143
                |:||||  :|:|:|:|||||||| :|: ||||| ||||||||:: :|||||  ||||||:
Db          79  LSAAHCFPSEHHKEAYEVKLGAHQLDSYSEDAKVSTLKDIIPHPSYIQEGSQGDIALLQL  138

Qy         144  QFPLTPSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMS-DILLQASVQVIDSTR  202
                :||||   :|||| |||:||||||  ||| |||| :|||||||  :||:|||:||:|: |
Db         139  SRPITPSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRET  198

Qy         203  CNA---DDAYQGE---VTEKMMCAGIPEGGVDTCQGDSGGPLMYQSD-QWHVVGIVSWGY  255
                ||:    ||||| ||  ||:|  ||  |:| | |||:||||:||||  ||:| ||:||||
Db         199  CNCLYNIDAKPEBPHFVQEDMVCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGD  258

Qy         256  GCGGPSTPGVYTKVSAYLNWIY-----------NVWKAEL--SRHHHHHH  291
                |||||||||||||||||||||            ||||||   |||||||
Db         259  ACGARNRPGVYTLASSYASWIQSKVTELQPRVVPQTOESQPDSNLCGSHLAFSSRHHHHH  318

Qy         292  H  292
                |
Db         319  H  319
```

```
RESULT 11
US-09-386-642-54
;  Sequence 54, Application US/09386642
;  Patent No. 6420157
;  GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Zymogen Activation System
;  FILE REFERENCE: ORT-1028
;  CURRENT APPLICATION NUMBER: US/09/386,642
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
;
;  SEQ ID NO 54
;  LENGTH: 284
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Human MH2
;  OTHER INFORMATION: protease in PFEK zymogen vector
US-09-386-642-54

Query Match             35.9%;  Score 574;  DB 4;  Length 284;
Best Local Similarity   44.2%;  Pred. No. 1.1e-53;
Matches   133;  Conservative   39;  Mismatches  103;  Indels   26;  Gaps   11;
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Qy           1  MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGY-ALD  59
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Db           1  MDSKGSSQKSRLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYNCLE  60

Qy          60  VDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL--GSFPS  117
                  ||| ||:  :||||  ||  :|||   |:|:|  |||  ||:  :|:|  ||  |||
Db          61  PHSQPWQAALVMENELFCSGVLVHPQWYLSAAHCFQN----SYTIGLGLHSLEADQPEG  115

Qy         118  LAVAKIIIEBNPMYPKD--NDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWII  174
                  :|||| |:||||||   ||||||:   ||:|||| ||||| :|||||:||||:::
Db         116  SQMVEASLSVRHPEYNRPLLANDLMLIKLDESVESDTIRSISIA--SQCPTAGNSCLVS  173

Qy         175  GWGFTKQNGGKMSDILLQASVQVIDSTRCNA-DDAYQGEVTEKMMCAGIPEGGVDTCQG  232
                |||| |||   |  :||:|||:|::: |||| ||||||||:||   |||||||||:|||
Db         174  GWGLLA--NGRMPTVLQCVNVSVVSEEVCSKLYDPLYH---PSMFCAGGGHDQKDSCNG  227

Qy         233  DSGGPLMYQSDQWHVVGIVSWGYG-CGGPSTPGVYTKVSAYLNWIYNVWKAELSRHHHHH  291
                |||||   ||: ||:| ||:|| | |||||||||||||||||| :||||||| :|||||
Db         228  DSGGPLICNG---YLQCLVSFGKAPCQGVGVPGVYTNLCKFTEWIEKTVQAS-SRHHHHH  283

Qy         292  H  292
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Db         284  H  284
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RESULT 12
US-08-508-448C-25
;  Sequence 25, Application US/08508448C
;  Patent No. 5804410
;  GENERAL INFORMATION:
;  APPLICANT: Kazuyoshi YAMAOKA et al.
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
;  TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
;  NUMBER OF SEQUENCES: 25
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Wenderoth, Lind & Ponack
;     STREET: 805 Fifteenth Street, N.W., #700
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: Wordperfect 5.1
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/508,448C
;     FILING DATE: July 28, 1995
;     CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Warren M. Cheek, Jr.
;     REGISTRATION NUMBER: 33,367
;     REFERENCE/DOCKET NUMBER:
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-371-8850
;     TELEFAX:
;     TELEX:
;  INFORMATION FOR SEQ ID NO: 25:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 418 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
US-08-508-448C-25

Query Match             32.9%;  Score 526.5;  DB 1;  Length 418;
Best Local Similarity   41.8%;  Pred. No. 2.5e-48;
Matches    97;  Conservative   49;  Mismatches   79;  Indels    7;  Gaps    4;
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;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
;
SEQ ID NO 83
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-370-838-83

Query Match             32.9%;  Score 526.5;  DB 4;  Length 418;
Best Local Similarity   41.8%;  Pred. No. 2.5e-48;
Matches    97;  Conservative   49;  Mismatches   79;  Indels    7;  Gaps    4;

Qy     49  DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG 108
               : :||:||  |||||||||:::  :|||||||| ::: :| ::
Db    184  EQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNMWILTAAHCFRSNSNPRDWIATSG 243

Qy    109  SDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQPPLTFSGTVRPICLPFFDEELT 166
               |||:|  :||:: :||  ::||| :|:: :||
Db    244  IST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP 301

Qy    167  PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG 226
               |: :: :|| :||| |:  |:: :  |||:|||:|:|:||
Db    302  PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG 360

Qy    227  VDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI 276
               ||||||||||||||:::  :||||||||||||||:||:|:|:|||
Db    361  VDACQGDSGGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWI 412


RESULT 15
US-09-370-838-62
;   Sequence 62, Application US/09370838
;   Patent No. 644425
;   GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
;
SEQ ID NO 62
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-370-838-62

Query Match             32.8%;  Score 524.5;  DB 4;  Length 418;
Best Local Similarity   41.4%;  Pred. No. 4.1e-48;
Matches    96;  Conservative   50;  Mismatches   79;  Indels    7;  Gaps    4;

Qy     49  DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG 108
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Db    184  EQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNMWILTAAHCFRSNSNPRDWIATSG 243

Qy    109  SDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQPPLTFSGTVRPICLPFFDEELT 166
               |||:|  :||:: :||  ::||| :|:: :||
Db    244  IST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP 301

Qy    167  PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG 226
               |: :: :|| :||| |:  |:: :  |||:|||:|:|:||
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```
Qy     49  DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG 108
               : :||:||  |||||||||:::  :|||||||| ::: :| ::
Db    184  EQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNMWILTAAHCFRSNSNPRDWIATSG 243

Qy    109  SDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQPPLTFSGTVRPICLPFFDEELT 166
               |||:|  :||:: :||  ::||| :|:: :||
Db    244  IST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP 301

Qy    167  PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG 226
               |: :: :|| :||| |:  |:: :  |||:|||:|:|:||
Db    302  PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG 360

Qy    227  VDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI 276
               ||||||||||||||:::  :||||||||||||||:||:|:|:|||
Db    361  VDACQGDSGGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWI 412


RESULT 13
US-09-370-838-82
;   Sequence 82, Application US/09370838
;   Patent No. 644425
;   GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
;
SEQ ID NO 82
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-370-838-82

Query Match             32.9%;  Score 526.5;  DB 4;  Length 418;
Best Local Similarity   41.8%;  Pred. No. 2.5e-48;
Matches    97;  Conservative   49;  Mismatches   79;  Indels    7;  Gaps    4;

Qy     49  DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG 108
               : :||:||  |||||||||:::  :|||||||| ::: :| ::
Db    184  EQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNMWILTAAHCFRSNSNPRDWIATSG 243

Qy    109  SDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQPPLTFSGTVRPICLPFFDEELT 166
               |||:|  :||:: :||  ::||| :|:: :||
Db    244  IST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP 301

Qy    167  PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG 226
               |: :: :|| :||| |:  |:: :  |||:|||:|:|:||
Db    302  PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG 360

Qy    227  VDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI 276
               ||||||||||||||:::  :||||||||||||||:||:|:|:|||
Db    361  VDACQGDSGGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWI 412


RESULT 14
US-09-370-838-83
;   Sequence 83, Application US/09370838
;   Patent No. 644425
;   GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
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Db   302 PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG 360

Qy   227 VDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI 276
             || ||||||||| : : | ||||| :| ||||: |: |||::||
Db   361 VDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYIDWI 412

Search completed: December 2, 2003, 02:31:10
Job time : 22.2875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:42:05 ; Search time 262.68 Seconds
                                       (without alignments)
                                       3662.446 Million cell updates/sec

Title: US-09-607-745-9
Perfect score: 1600
Sequence: 1 MDSKGSSQKSRLLLLJVVSN........LNWIYNVWKAELSRHHHHHH 292

Scoring table: BLOSUM62

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    Ygapop 10.0 , Ygapext 0.5
    Fgapop   6.0 , Fgapext 7.0
    Delop   6.0 , Delext   7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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-LOOPCL=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09607745 @CGN_1_1_129 @runat_01122003_160940_10006
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Published Applications NA:*
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 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1266	79.1	2038	12	US-10-180-719-18	Sequence 18, Appl
2	1266	79.1	2063	11	US-09-888-257A-2	Sequence 2, Appli
3	1266	79.1	2063	11	US-09-946-374-2	Sequence 274, App
4	1266	79.1	2063	12	US-10-015-387A-274	Sequence 274, App
5	1266	79.1	2063	12	US-10-063-735-111	Sequence 111, App
6	1266	79.1	2063	12	US-10-006-130A-274	Sequence 274, App
7	1266	79.1	2063	12	US-10-199-672-329	Sequence 329, App
8	1266	79.1	2063	12	US-10-006-172A-274	Sequence 274, App
9	1266	79.1	2063	12	US-10-187-749-329	Sequence 329, App
10	1266	79.1	2063	12	US-10-194-457-329	Sequence 329, App
11	1266	79.1	2063	12	US-10-184-642-329	Sequence 329, App
12	1266	79.1	2063	12	US-10-196-747-329	Sequence 329, App
13	1266	79.1	2063	12	US-10-015-392A-274	Sequence 274, App
14	1266	79.1	2063	12	US-10-017-253A-274	Sequence 274, App
15	1266	79.1	2063	12	US-10-173-689-329	Sequence 329, App
16	1266	79.1	2063	12	US-10-173-690-329	Sequence 329, App
17	1266	79.1	2063	12	US-10-173-691-329	Sequence 329, App
18	1266	79.1	2063	12	US-10-173-692-329	Sequence 329, App
19	1266	79.1	2063	12	US-10-173-694-329	Sequence 329, App
20	1266	79.1	2063	12	US-10-173-698-329	Sequence 329, App
21	1266	79.1	2063	12	US-10-173-699-329	Sequence 329, App
22	1266	79.1	2063	12	US-10-173-707-329	Sequence 329, App
23	1266	79.1	2063	12	US-10-174-569-329	Sequence 329, App
24	1266	79.1	2063	12	US-10-174-583-329	Sequence 329, App
25	1266	79.1	2063	12	US-10-174-587-329	Sequence 329, App
26	1266	79.1	2063	12	US-10-174-589-329	Sequence 329, App
27	1266	79.1	2063	12	US-10-174-591-329	Sequence 329, App
28	1266	79.1	2063	12	US-10-175-736-329	Sequence 329, App
29	1266	79.1	2063	12	US-10-175-742-329	Sequence 329, App
30	1266	79.1	2063	12	US-10-175-744-329	Sequence 329, App
31	1266	79.1	2063	12	US-10-175-745-329	Sequence 329, App
32	1266	79.1	2063	12	US-10-175-748-329	Sequence 329, App
33	1266	79.1	2063	12	US-10-175-751-329	Sequence 329, App
34	1266	79.1	2063	12	US-10-175-754-329	Sequence 329, App
35	1266	79.1	2063	12	US-10-176-480-329	Sequence 329, App
36	1266	79.1	2063	12	US-10-176-489-329	Sequence 329, App
37	1266	79.1	2063	12	US-10-176-754-329	Sequence 329, App
38	1266	79.1	2063	12	US-10-176-755-329	Sequence 329, App
39	1266	79.1	2063	12	US-10-176-759-329	Sequence 329, App
40	1266	79.1	2063	12	US-10-176-920-329	Sequence 329, App
41	1266	79.1	2063	12	US-10-176-922-329	Sequence 329, App
42	1266	79.1	2063	12	US-10-176-924-329	Sequence 329, App
43	1266	79.1	2063	12	US-10-176-984-329	Sequence 329, App
44	1266	79.1	2063	12	US-10-179-508-329	Sequence 329, App
45	1266	79.1	2063	12	US-10-179-512-329	Sequence 329, App

ALIGNMENTS

RESULT 1
US-10-180-719-18
; Sequence 18, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;   Hillman, Jennifer L.
;   Yue, Henry
;   Guegler, Karl J.
;   Corley, Neil C.
;   Tang, Tom Y.
;   Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Dr.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS

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              SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/10/180,719
;         FILING DATE: 25-Jun-2002
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US/09/008,271
;         FILING DATE: 16-Jan-1998
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Mohan-Peterson, Sheela
;         REGISTRATION NUMBER: 41,201
;         REFERENCE/DOCKET NUMBER: PF-0458 US
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 650-855-0555
;         TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 2038 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;         LIBRARY: COLNNOT13
;         CLONE: 1337018
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-180-719-18

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Pred. No.:                      1.64e-152       Length:           2038
Score:                          1266.00         Matches:           228
Percent Similarity:             98.29%          Conservative:        2
Best Local Similarity:          97.44%          Mismatches:          4
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US-09-607-745-9 (1-292)   x US-10-180-719-18  (1-2038)

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Qy     71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpProValLeuThrAla  90
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Db    863 TACGACAAACAGCACGTTCTGTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA  922

Qy     91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp  110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    923 GCCCACTGCTTCAGGAAACATACGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC  982

Qy    111 LysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleGluGluAsnPro  130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    983 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCGCAAGATCATCATCATTGAATTCAACCCC  1042

Qy    131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer  150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA  1102

Qy    151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro  170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA  1162

Qy    171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu  190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG  1222

Qy    191 LeuGlnAlaSerValGlnInValIleIleAspSerThrArgCysAsnAlaAspAlaTyrGln  210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1223 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCCGATGCGTACCAG  1282

Qy    211 GlyGluValThrGluLysMetCysAlaGlyTyrLeuProGluGlyGlyValAspThrCys  230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1283 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGGTACCTGCCAGAGGGGTGGACACCTGC  1342

Qy    231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle  250
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                                    Db 1343 CAGGGTGACAGTGTGGGCCCTGATGTGTGGGCCCTGATGTGTGGGCCCTGACCAGTGACCAATCTGACCAGTGGTGGGCATC 1402
                                    Qy   251 ValSerTrpGlyTyrGlyCysGlyAlaTyrGlyProSerThrProGlyValTyrLysValSer 270
                                    Db 1403 GTTAGCTGGGGCTATGGCTGCGGCGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1462
                                    Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
                                    Db 1463 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1504

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RESULT 2
US-09-888-257A-2
;  Sequence 2, Application US/09888257A
;  Publication No. US20030060612A1
;  GENERAL INFORMATION:
;       APPLICANT: Goddard, Audrey
;       APPLICANT: Godowski, Paul J.
;       APPLICANT: Gurney, Austin L.
;       APPLICANT: Hillan, Kenneth J.
;       APPLICANT: Polakis, Paul
;       APPLICANT: Smith, Victoria
;       APPLICANT: Wood, William I.
;       APPLICANT: Wu, Thomas D.
;       APPLICANT: Zhang, Zemin
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF TUMOR
;  FILE REFERENCE: P5002R1
;  CURRENT APPLICATION NUMBER: US/09/888,257A
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/063,540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20111
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: US 60/089,653
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: US 60/099,792
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04342
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/103,678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR APPLICATION NUMBER: US 60/235,451
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06666
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
;      LENGTH: 2063
;      TYPE: DNA
;      ORGANISM: Homo Sapien
US-09-888-257A-2

Alignment Scores:
Pred. No.:                      1.67e-152       Length:           2063
Score:                          1266.00         Matches:           228
Percent Similarity:             98.29%          Conservative:        2
Best Local Similarity:          97.44%          Mismatches:          4
Query Match:                    79.12%          Indels:              0
DB:                             11              Gaps:                0
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US-09-607-745-9 (1-292) x US-09-888-257A-2 (1-2063)

```
Qy        51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
             ::::::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       804 CGTGTGGTGGTGGTGGGAGGAGGGCCTCTGTGGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy        71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCCTCACGGCA 923

Qy        91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy       111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 130
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy       131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTTCCTCA 1103

Qy       151 GlyThrValArgProIleCysLeuProPheAspGluGlnLeuThrProAlaThrPro 170
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy       171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1164 CTCTGGATCATTGATGGGGCTTTACGAAGCAGAAGATGAGGAAGATGTCTGACATACTG 1223

Qy       191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1224 CTGCAGGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAG 1283

Qy       211 GlyGluValThrGluLysMetMetCysSerAlaGlyIleProGluGlyGlyValAspThrCys 230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy       231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC 1403

Qy       251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy       271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu 284
             ||||||||||||||||||||||||||||||||||||||||||
Db      1464 GCCTATCTCAACTGATCTACAAATGTCTGGAAGGCTGAGCTG 1505
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RESULT 3
US-09-946-374-274
; Sequence 274, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
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; PRIOR APPLICATION NUMBER: 60/099808
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; PRIOR APPLICATION NUMBER: 60/100627
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; PRIOR APPLICATION NUMBER: 60/100662
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; PRIOR APPLICATION NUMBER: 60/100711
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; PRIOR APPLICATION NUMBER: 60/100848

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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
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; PRIOR APPLICATION NUMBER: 60/100919
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102570
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; PRIOR APPLICATION NUMBER: 60/102571
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; PRIOR APPLICATION NUMBER: 60/103258
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; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
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; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
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; PRIOR APPLICATION NUMBER: 60/103678
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; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-26
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Alignment Scores:
Pred. No.:                              1.67e-152        Length:        2063
Score:                                  1266.00          Matches:       228
Percent Similarity:                     98.29%           Conservative:  2
Best Local Similarity:                  97.44%           Mismatches:    4
Query Match:                            79.12%           Indels:        0
DB:                                     11               Gaps:          0

US-09-607-745-9 (1-292) x US-09-946-374-274 (1-2063)

US-09-607-745-9  (1-292)  x US-09-946-374-274  (1-2063)

Qy      51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln  70
           ::::::||||||||
Db     804 CGTGTGGTGGGTGGGGAGGAGGCCCTCGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy      71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla  90
                                     ||||||||||||||||||||||||||||||
Db     864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy      91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
                                     |||||||||||||||||||||||||||||||
Db     924 GCCCACTGTCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy     111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluProAsnPro 130
                                     ||||||||||||||||||||||||||||||
Db     984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy     131 MetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheProLeuThrPheSer 150
                                     ||||||||||||||||||||||||||||||
Db    1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy     151 GlyThrValArgProIleCysLeuProPheAspGluGluThrProAlaThrPro 170
                                     |||||||||||||||||||||||||||
Db    1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy     171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
                                     |||||||||||||||||||||||||||
Db    1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGCAGAATGAGGGAAGATGTCTGACATACTG 1223

Qy     191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
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Db  1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAG 1283

Qy   211 GlyGluValThrGluLysMetMetCysAlaGlyIleLeuProGluGluGlyGlyValAspThrCys 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 GGGGAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344 CAGGGTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGGTGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
         ||||||||||||||||||||||||||||||||||||||||||
Db  1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
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RESULT 4
US-10-015-387A-274
; Sequence 274, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-274

Alignment Scores:
Pred. No.:
Score: 1266.00
Percent Similarity: 98.29%
Best Local Similarity: 97.44%
Query Match: 79.12%
DB:

Length:	2063
Matches:	228
Conservative:	2
Mismatches:	4
Indels:	0
Gaps:	0

1.67e-152

US-09-607-745-9 (1-292) x US-10-015-387A-274 (1-2063)

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Qy    51 LysIleValGlyGlyTyrAlaLeuAspSerTrpProTrpGlnValSerIleGln 70
         ::::|||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CGTGTGGTGGGTGGGGAGGAGGCCTCTTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy    71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy    91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 GCCCACTGCTTCAGGAAGCATACCGATGTGTTCAACTGGAAAGTGCGGGCAGGCTCAGAC 983
```

```
Qy   111 LysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleIleGluPheAsnPro 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy   131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044 ATGTACCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy   151 GlyThrValArgProIleCysLeuProPheGluGluLeuThrProAlaThrPro 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCCAGCCACCCCA 1163

Qy   171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyThrLysAspIleLeu 190
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164 CTCTGGATCATTGGATGGGGCTTTACGAACCAGAATGGAGGGAAGATGTCTGACATACTG 1223

Qy   191 LeuGlnAlaSerValGlnValIleAspAspThrArgCysAsnAlaAspAlaTyrGln 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGTACCAG 1283

Qy   211 GlyGlyValThrGluLysMetMetCysAlaGlyIleLeuProGluGluGlyGlyValAspThrCys 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 GGGGAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344 CAGGGTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGGTGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
         ||||||||||||||||||||||||||||||||||||||||||
Db  1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
```

RESULT 5
US-10-063-735-111
; Sequence 111, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2830R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 111
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-735-111

Alignment Scores:
Pred. No.:
Score: 1266.00
Percent Similarity: 98.29%
Best Local Similarity: 97.44%
Query Match: 79.12%
DB:

Length:	2063
Matches:	228
Conservative:	2
Mismatches:	4
Indels:	0
Gaps:	0

1.67e-152

US-09-607-745-9 (1-292) x US-10-063-735-111 (1-2063)

```
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-274

Alignment Scores:
Pred. No.:                 1.67e-152        Length:        2063
Score:                     1266.00          Matches:       2063
Percent Similarity:        98.29%           Conservative:   228
Best Local Similarity:     97.44%           Mismatches:       2
Query Match:               79.12%           Indels:           4
DB:                        12               Gaps:             0
```

US-09-607-745-9 (1-292) x US-10-006-130A-274 (1-2063)

```
Qy    51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
         :::::::||||||
Db   804 CGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGCAGGTCAGCATCCAG 863

Qy    71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
         ||||||||||||
Db   864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy    91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
         ||||||||||||
Db   924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTTCAGAC 983

Qy   111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 130
         ||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTGAATTCAACCCC 1043

Qy   131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
         ||||||||||||
Db  1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy   151 GlyThrValArgProIleCysLeuProPheAspGluLeuProAlaThrPro 170
         ||||||||||||
Db  1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTTGATGAGGAGCTCCCAGCCACCCCA 1163

Qy   171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
         ||||||||||||
Db  1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG 1223

Qy   191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
         ||||||||||||
Db  1224 CTGCAGGCCGTCAGTTCCAGGTCATTGACAGCACACGGTGCAATGCAGATGCGTACCAG 1283

Qy   211 GlyGluValThrGluLysMetCysAlaGlyTyrIleProGluGlyGlyValAspThrCys 230
         ||||||||||||
Db  1284 GGGGAAGTCACCGAGAAGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspAsnTrpHisValValGlyIle 250
         ||||||||||||
Db  1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACAATTGGCATGTGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         ||||||||||||
Db  1404 GTTAGCTGGGGCTATGGCTGCGGGGGGCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
         ||||||||||||
Db  1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
```

RESULT 6
US-10-006-130A-274
; Sequence 274, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm

RESULT 7
US-10-199-672-329
; Sequence 329, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc

```
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/199,672
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE:  2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE:  1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE:  1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE:  1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE:  1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE:  1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE:  1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE:  1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE:  1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE:  1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
;
;  SEQ ID NO 329
;  LENGTH: 2063
;  TYPE: DNA
;  ORGANISM: Homo Sapien
us-10-199-672-329

Alignment Scores:
Pred. No.:
Score:                    1266.00
Percent Similarity:       98.29%
Best Local Similarity:    97.44%
Query Match:              79.12%
DB:                       12

Length:        2063
Matches:       228
Conservative:  2
Mismatches:    4
Indels:        0
Gaps:          0

US-09-607-745-9 (1-292) x US-10-199-672-329 (1-2063)

Qy  51  LysIleValIleGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln  70
            ::::::||||||
Db 804  CGTGTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCCTGGCAGGTCAGCATCCAG  863

Qy  71  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisValLeuThrAla  90
            ||||||
Db 864  TACGACAAACAGCACAGTGCTCTGGAGGGAGCATCCTGGGACCCCCACTGGGTCCTCACGGCA  923

Qy  91  AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp  110
            ||||||
Db 924  GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC  983

Qy 111  LysLeuGlySerPheProSerLeuAlaValAlaLysLysIleIleIleGluIleGluAsnPro  130
            ||||||
Db 984  AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC  1043

Qy 131  MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnHisProLeuThrPheSer  150
            ||||||
Db 1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTCCAGTTCCCACTCACTTTCTCA  1103

Qy 151  GlyThrValArgProIleCysLeuProProPheAspPheAspGluThrProAlaThrPro  170
            ||||||
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```
Db 1104 GGCACAGTCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGTCACTCCAGCCACCCA  1163

Qy 171  LeuTrpIleIleGlyTrpGlyPheLysGlyGlnAsnGlyGlyLysMetSerAspIleLeu  190
            |||||||||||
Db 1164 CTCTGGATCATTGGATGGGGCTTTAAGGGCCAGAATGGAGGAAGATGTCTGACATACTG  1223

Qy 191  LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln  210
            |||||||||||
Db 1224 CTGCAGGCGGTCAGTCCAGGTCATTGACACAGCACACGGTGCAATGCAGACGATGCGTACCAG  1283

Qy 211  GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys  230
            |||||||||||
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGCGCAGGCATCCCGGAGGGGGTGGACACCTGC  1343

Qy 231  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle  250
            |||||||||||
Db 1344 CAGGGTGACAGTGGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC  1403

Qy 251  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer  270
            |||||||||||
Db 1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCAGCACCCCAGGAGTATACACCAAGGTCTCA  1463

Qy 271  AlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeu  284
            |||||||||||
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG  1505


RESULT 8
US-10-006-172A-274
;  Sequence 274, Application US/10006172A
;  Publication No. US20030153000A1
;  GENERAL INFORMATION:
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C11
;  CURRENT APPLICATION NUMBER: US/10/006,172A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
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PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: 60/100388
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PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24

PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24
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PRIOR APPLICATION NUMBER: 60/102687
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PRIOR APPLICATION NUMBER: 60/102965
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PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07
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PRIOR APPLICATION NUMBER: 60/105104
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694

; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 329
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-329

Alignment Scores:
Pred.No.:
Score: 1.67e-152   Length: 2063
Percent Similarity: 98.29%   Matches: 228
Best Local Similarity: 97.44%   Conservative: 2
Query Match: 79.12%   Mismatches: 4
DB: 12   Indels: 0
                                              Gaps: 0

US-09-607-745-9 (1-292) x US-10-187-749-329 (1-2063)

Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
         :::::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CGTGTGGTGGGTGGGGAGGAGGCCCTTGTGGATTCTTGGCCTTGGCAGTGTCAGCATCCAG 863

Qy   71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCCAGGGCTTCAGAC 983

Qy   111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCCTGGCCGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy   131 MetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheProLeuThrPheSer 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

US-10-187-749-329

; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Alignment Scores:
Pred.No.:
Score: 1.67e-152   Length: 2063
Percent Similarity: 98.29%   Matches: 228
Best Local Similarity: 97.44%   Conservative: 4
Query Match: 79.12%   Mismatches:
DB: 12   Indels: 0
                                              Gaps: 0

US-09-607-745-9 (1-292) x US-10-006-1724-274 (1-2063)

Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
         :::::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CGTGTGGTGGGTGGGGAGGAGGCCCTTGTGGATTCTTGGCCTTGGCAGTGTCAGCATCCAG 863

Qy   71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCCAGGGCTTCAGAC 983

Qy   111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCCTGGCCGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy   131 MetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheProLeuThrPheSer 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy   151 GlyThrValArgProIleCysLeuProPhePheAspGluPheAspGluLeuThrProAlaThrPro 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1104 GGCACAGTGCAGGCCCCATCTGCTCGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCCA 1163

Qy   171 LeuTrpIleIleGlyTyrTrpGlyPheThrLysSerGlnAsnGlyGlyLysMetSerAspIleLeu 190
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1164 CTCTGGATCATTGGATAGGGGGCTTTACGAAGCAGAAATGAGCGGAAGATGTCTGACATACTG 1223

Qy   191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1224 CTGCAGGGCTGCAGTCCAGGTCAGTTGTCGGCCCCTGATGTACCAATCTGACCAGAGACCAATGCCTACCAG 1283

Qy   211 GlyGluValThrGluLysMetMetCysAlaGlyTyrIleProGluGlyTyrGlyValAspThrCys 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1344 CAGGGTGACAGTGGTGGCCCCCGATGTACCAATCTGACCAGTGGCATGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerGlyGlyProGlyValTyrThrLysValSer 270
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACGCCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
         ||||||||||||||||||||||||||||||||||||||||||
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

RESULT 9
US-10-187-749-329
; Sequence 329, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:

Qy   151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1104 GGCACAGTCAGGCCCATCTGCTGCCCTTCTTCGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy   171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGGAAGATGTCTGACATACTG 1223

Qy   191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAATGCGATGCGTACCAG 1283

Qy   211 GlyGluValThrGluHisLysMetMetCysAlaGlyIleProGluGlyGlyValGlyValAspThrCys 230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1284 GGGGAAGTCACCGAGAGATGATGTGTCAGGCATCCCCGAAGGGGGTGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspAsnTrpHisValValGlyIle 250
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1344 CAGGGTGACAGTGGTGGCCCCTGATGTACCAATCTGACCAGTGCATGTGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1404 GTTAGCTGGGGCTATGGCTGGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu 284
         |||||||||||||||||||||||||||||||||||||||
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

RESULT 10
US-10-194-457-329
;
; Sequence 329, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Chen,Jian
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Pan,James
;   APPLICANT: Smith,Victoria
;   APPLICANT: Watanabe,Colin K.
;   APPLICANT: Wood,William I.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3430R1C296
;   CURRENT APPLICATION NUMBER: US/10/194,457
;   CURRENT FILING DATE: 2002-07-11
;   PRIOR APPLICATION NUMBER: 10/052586
;   PRIOR FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/059266
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/063120
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063121
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063486
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063540
;   PRIOR FILING DATE: 1997-10-21
;   PRIOR APPLICATION NUMBER: 60/063541
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063544
;   PRIOR FILING DATE: 1997-10-28
;   Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 612
;   SEQ ID NO 329

;   LENGTH: 2063
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-194-457-329

Alignment Scores:
Pred. No.:   Length: 2063
1.67e-152   Matches: 228
Score: 1266.00   Conservative: 2
Percent Similarity: 98.29%   Mismatches: 4
Best Local Similarity: 97.44% Indels: 0
Query Match: 79.12%   Gaps: 0
DB: 12

US-09-607-745-9 (1-292) x US-10-194-457-329 (1-2063)

Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspAspTrpProTrpGlnValSerIleGln 70
         :::::::|||||||||||||||||||||||||||||||||||||||||||||
Db   804 CGTGTGGGTGGGTGGGGAGGGCCCTCTGTGGATTCTTGGCCTTGGCAGTCAGCATCCAG 863

Qy   71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 TACGACAAACAGCACAGTGTCTGTGGAGGAGCATCCTGACCCCCACTGGGTCCTCACGGCA 923

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy   111 LysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleIleGluPheAsnPro 130
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCCTGGCCGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy   131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrPheSer 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1044 ATGTACCCCAAAGACAATGACATGGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy   151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1104 GGCACAGTCAGGCCCATCTGCCTGCCCTTCTTCGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy   171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGGAAGATGTCTGACATACTG 1223

Qy   191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAG 1283

Qy   211 GlyGluValThrGluHisLysMetMetCysAlaGlyIleProGluGlyGlyValGlyValIle 230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGCAGGCATCCCCGAAGGGGGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspAsnTrpHisValValGlyIle 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1344 CAGGGTGACAGTGGTGGCCCCCTGATGTACCAGTCGGACAATTGGCATGTGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSerLeu 270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1404 GTTAGCTGGGGCTATGGCTGTGGGGGGCCCAGCACCCCAGGAGTGGGCATC 1463

Qy   191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAG 1283

Qy   211 GlyGluValThrGluHisLysMetMetCysAlaGlyIleProGluGlyGlyValGlyValIle 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGCAGGCATCCCCGAAGGGGGTGGACACCTGC 1343

Qy   231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspAsnTrpHisValValGlyIle 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1344 CAGGGTGACAGTGGTGGCCCCCTGATGTACCAGTCGGACAATTGGCATGTGGTGGGCATC 1403

Qy   251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1404 GTTAGCTGGGGCTATGGCTGTGGGGGGCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy   271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu 284
         |||||||||||||||||||||||||||||||||||||||
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

RESULT 11
US-10-184-642-329
;
; Sequence 329, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Chen,Jian
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.

```
;   APPLICANT:  Gurney,Austin L.
;   APPLICANT:  Pan,James
;   APPLICANT:  Smith,Victoria
;   APPLICANT:  Watanabe,Colin K.
;   APPLICANT:  Wood,William I.
;   APPLICANT:  Zhang,Zemin
;   TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;   FILE REFERENCE:  P3430R1C194
;   CURRENT APPLICATION NUMBER:  US/10/184,642
;   CURRENT FILING DATE:  2002-06-27
;   Prior Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS:  612
;   SEQ ID NO 329
;   LENGTH:  2063
;   TYPE:  DNA
;   ORGANISM:  Homo Sapien
US-10-184-642-329

Alignment Scores:
Pred. No.:                 1.67e-152          Length:          2063
Score:                     1266.00            Matches:         228
Percent Similarity:        98.29%             Conservative:    2
Best Local Similarity:     97.44%             Mismatches:      4
Query Match:               79.12%             Indels:          0
DB:                        12                 Gaps:            0

US-09-607-745-9 (1-292) x US-10-184-642-329 (1-2063)

Qy     51 LysIleValGlyGlyTyrAlaLeuAspSerTrpProTrpGlnValSerIleGln 70
          ::::::|||||||||||||||||||||||||||||||||||||||||||||||
Db    804 CGTGTGGTGGGTGGGGGAGGAGGCCCTCGTGTGGATTCTTGGCCTTGGCCAGGTCAGCATCCAG 863

Qy     71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy     91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy    111 LysLeuGlyLysLeuGlySerPheProSerLeuAlaValAlaValAlaLysIleIleIleGluPheAsnPro 130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTGAATTCAACCCC 1043

Qy    131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy    151 GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro 170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy    171 LeuTrpIleIleGlyTyrTrpLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAAATGTCTGACATACTG 1223

Qy    191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 CTGCAGGCGGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGATGCCTACCAG 1283

Qy    211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAGGGGGTGGACACCTGC 1343

Qy    231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerGlnTrpHisValValGlyIle 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAAATCTGACCAGTGCATGTGGTGGGCATC 1403

Qy    251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy    271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
          ||||||||||||||||||||||||||||||||||||||||||
Db   1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
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```
RESULT 12
US-10-196-747-329
; Sequence 329, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
;   APPLICANT:  Baker,Kevin P.
;   APPLICANT:  Chen,Jian
;   APPLICANT:  Desnoyers,Luc
;   APPLICANT:  Godard,Audrey
;   APPLICANT:  Godowski,Paul J.
;   APPLICANT:  Gurney,Austin L.
;   APPLICANT:  Pan,James
;   APPLICANT:  Smith,Victoria
;   APPLICANT:  Watanabe,Colin K.
;   APPLICANT:  Wood,William I.
;   APPLICANT:  Zhang,Zemin
;   TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;   FILE REFERENCE:  P3430R1C346
;   CURRENT APPLICATION NUMBER:  US/10/196,747
;   CURRENT FILING DATE:  2002-07-16
;   Prior Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS:  612
; SEQ ID NO 329
;   LENGTH:  2063
;   TYPE:  DNA
; ORGANISM:  Homo Sapien
US-10-196-747-329

Alignment Scores:
Pred. No.:                 1.67e-152          Length:          2063
Score:                     1266.00            Matches:         228
Percent Similarity:        98.29%             Conservative:    2
Best Local Similarity:     97.44%             Mismatches:      4
Query Match:               79.12%             Indels:          0
DB:                        12                 Gaps:            0

US-09-607-745-9 (1-292) x US-10-196-747-329 (1-2063)

Qy     51 LysIleValGlyGlyTyrAlaLeuAspSerTrpProTrpGlnValSerIleGln 70
          ::::::|||||||||||||||||||||||||||||||||||||||||||||||
Db    804 CGTGTGGTGGGTGGGGGAGGAGGCCCTCGTGTGGATTCTTGGCCTTGGCCAGGTCAGCATCCAG 863

Qy     71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy     91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy    111 LysLeuGlySerPheProSerLeuAlaValAlaValAlaLysIleIleIleGluPheAsnPro 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTGAATTCAACCCC 1043

Qy    131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy    151 GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro 170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy    171 LeuTrpIleIleGlyTyrTrpLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAAATGTCTGACATACTG 1223

Qy    191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 CTGCAGGCGGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGATGCCTACCAG 1283
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Percent Similarity:        98.29%          Conservative:  2
Best Local Similarity:     97.44%          Mismatches:    4
Query Match:               79.12%          Indels:        0
DB:                        12              Gaps:          0
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US-09-607-745-9 (1-292) x US-10-015-392A-274 (1-2063)

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Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln  70
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Db  804 CGTGTGGTGGGTGGGGAGGAGGGCCTCTGGGATTCTTGGCCTTGGCAGGTCAGCATCCAG  863

Qy   71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla   90
Db  864 TACGACAAACAGCACAGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA  923

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp  110
Db  924 GCCCACTGCTTCAGGAAGCATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC  983

Qy  111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro  130
Db  984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy  131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer  150
Db 1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy  151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro    170
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTCGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy  171 LeuTrpIleIleGluTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu  190
Db 1164 CTCTGGATCATTGAGTGGGGCTTTACGAAGCAGAATGGAGGAAAGATGTCTGACATACTG 1223

Qy  191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrArgGln  210
Db 1224 CTGCAGGCGCTCAGTCCAGGTCATTGACACAGCACACGGTGCAATGCACGATGCGTACCAG 1283

Qy  211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyValGlyValAspThrCys 230
Db 1284 GGGGAAGTCACCGAGAAGAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1343

Qy  231 GlnGlyAspSerGlyGlyMetTyrGlnSerAspGlnTrpHisValValGlyIle        250
Db 1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC 1403

Qy  251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer  270
Db 1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy  271 AlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeu                 284
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG                   1505
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RESULT 13
US-10-015-392A-274
; Sequence 274, Application US/10015392A
; Publication No. US2003016690lA1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-392A-274

Alignment Scores:
Pred. No.:   1.67e-152   Length: 2063
Score: 1266.00   Matches: 228

RESULT 14
US-10-017-253A-274
; Sequence 274, Application US/10017253A
; Publication No. US2003016605A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

```
;   APPLICANT:  Paoni, Nicholas F.
;   TITLE OF INVENTION:  Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION:  Acids Encoding the Same
;   FILE REFERENCE:  P2830P1662
;   CURRENT APPLICATION NUMBER:  US/10/017,253A
;   CURRENT FILING DATE:  2001-12-13
;   PRIOR APPLICATION NUMBER:  60/098716
;   PRIOR APPLICATION FILING DATE:  1998-09-01
;   PRIOR APPLICATION NUMBER:  60/098723
;   PRIOR APPLICATION FILING DATE:  1998-09-01
;   PRIOR APPLICATION NUMBER:  60/098749
;   PRIOR APPLICATION FILING DATE:  1998-09-01
;   PRIOR APPLICATION NUMBER:  60/098750
;   PRIOR APPLICATION FILING DATE:  1998-09-01
;   PRIOR APPLICATION NUMBER:  60/098803
;   PRIOR APPLICATION FILING DATE:  1998-09-02
;   PRIOR APPLICATION NUMBER:  60/098821
;   PRIOR APPLICATION FILING DATE:  1998-09-02
;   PRIOR APPLICATION NUMBER:  60/098843
;   PRIOR APPLICATION FILING DATE:  1998-09-02
;   PRIOR APPLICATION NUMBER:  60/099536
;   PRIOR APPLICATION FILING DATE:  1998-09-09
;   PRIOR APPLICATION NUMBER:  60/099596
;   PRIOR APPLICATION FILING DATE:  1998-09-09
;   PRIOR APPLICATION NUMBER:  60/099598
;   PRIOR APPLICATION FILING DATE:  1998-09-09
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS:  477
;   SEQ ID NO 274
;   LENGTH:  2063
;   TYPE:  DNA
;   ORGANISM:  Homo sapiens
US-10-017-253A-274

Alignment Scores:
Pred. No.:                  1.67e-152           Length:               2063
Score:                      1266.00             Matches:              228
Percent Similarity:         98.29%              Conservative:         2
Best Local Similarity:      97.44%              Mismatches:           4
Query Match:                79.12%              Indels:               0
DB:                         12                  Gaps:                 0

US-09-607-745-9 (1-292) x US-10-017-253A-274 (1-2063)

Qy     51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
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Db    804 CGTGTGGTGGGTGGGGGAGGAGGCCCTCTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy     71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy     91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 GCCCACTGCTTCAGGAAACATCCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy    111 LysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleIleGluPheAsnPro 130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043

Qy    131 MetTyrProLysAspAsnProIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy    151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro 170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy    171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG 1223

Qy    191 LeuGlnAlaSerValGlnValIleIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 CTGCAGGCGGTCAGTCAGGTCATCATGACAGCACACGGTGCAATGCAGACGATGCGTACCAG 1283

Qy    211 GlyGluValThrGlyLysMetCysAlaGlyTyrIleProGluGluCysGlyValAspThrCys 230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 GGGGAAGTCACCGAGAAGATGATCGTGCAGGCATCCCGGAGGGGGTGTGGACACCTGC 1343

Qy    231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAAATCTGACCAGTGACATGTGGTGGGCATC 1403

Qy    251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404 GTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy    271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu 284
          |||||||||||||||||||||||||||||||||||||
Db   1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGTGGCTGAGCTG 1505

RESULT 15
US-10-173-689-329
;   Sequence 329, Application US/10173689
;   Publication No. US2003016610A1
;   GENERAL INFORMATION:
;   APPLICANT:  Baker,Kevin P.
;   APPLICANT:  Chen,Jian
;   APPLICANT:  Desnoyers,Luc
;   APPLICANT:  Godard,Audrey
;   APPLICANT:  Godowski,Paul J.
;   APPLICANT:  Gurney,Austin L.
;   APPLICANT:  Pan,James
;   APPLICANT:  Smith,Victoria
;   APPLICANT:  Watanabe,Colin K.
;   APPLICANT:  Wood,William I.
;   APPLICANT:  Zhang,Zemin
;   TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;   FILE REFERENCE:  P3430R1C10
;   CURRENT APPLICATION NUMBER:  US/10/173,689
;   CURRENT FILING DATE:  2002-06-17
;   Prior Application removed  - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS:  612
;   SEQ ID NO 329
;   LENGTH:  2063
;   TYPE:  DNA
;   ORGANISM:  Homo Sapien
US-10-173-689-329

Alignment Scores:
Pred. No.:                  1.67e-152           Length:               2063
Score:                      1266.00             Matches:              228
Percent Similarity:         98.29%              Conservative:         2
Best Local Similarity:      97.44%              Mismatches:           4
Query Match:                79.12%              Indels:               0
DB:                         12                  Gaps:                 0

US-09-607-745-9 (1-292) x US-10-173-689-329 (1-2063)

Qy     51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
             ::::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804 CGTGTGGTGGGTGGGGGAGGAGGCCCTCTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy     71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy     91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 GCCCACTGCTTCAGGAAACATCCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy    111 LysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleIleGluPheAsnPro 130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043
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Qy    131  MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer  150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044  ATGTACCCCAAAGACAATGACATGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA  1103

Qy    151  GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro  170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104  GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA  1163

Qy    171  LeuTrpIleIleGlyTrpPheThrLysGlnAsnGlyLysMetSerAspIleLeu  190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164  CTCCTGGATCATTGGAATGGGGGCTTTACGAAGCAGAATGGGGAGAATGTCTGACATACTG  1223

Qy    191  LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln  210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224  CTGCAGGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAG  1283

Qy    211  GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys  230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284  GGGGAAGTCACCGAGAAGATGATGTGTCAGGCATCCCGAAGGGGTGTGGACACCTGC  1343

Qy    231  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle  250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344  CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGGCATC  1403

Qy    251  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer  270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404  GTTAGCTGGGGCTATGCTGCGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA  1463

Qy    271  AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu  284
               ||||||||||||||||||||||||||||||||||
Db   1464  GCCTATCTCAACTGGATCTACACAATGTCTGGAAGGCTGAGCTG  1505
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Job time : 275.18 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:30:15 ; Search time 56.2311 Seconds
(without alignments)
2292.040 Million cell updates/sec

Title: US-09-607-745-9
Perfect score: 1600
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop   6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_p/US09607745/runat_01122003_160938_9959/app_query.fasta_1.1038
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Database :   Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1266	79.1	2038	3	US-09-008-271A-18	Sequence 18, Appl
2	1266	79.1	2079	4	US-09-656-002-1	Sequence 1, Appli
3	765	47.8	1130	4	US-09-387-375-8	Sequence 8, Appli
4	754.5	47.2	1130	4	US-09-386-653A-8	Sequence 8, Appli
5	746	46.6	1169	4	US-09-386-642-7	Sequence 7, Appli
6	740.5	46.3	1166	4	US-09-386-629-2	Sequence 2, Appli
7	672.5	42.0	1052	4	US-09-386-642-10	Sequence 10, Appl
8	645	40.3	1049	4	US-09-386-642-9	Sequence 9, Appli
9	601.5	37.6	1103	4	US-09-386-642-59	Sequence 59, Appl
10	593	37.1	1142	4	US-09-386-642-8	Sequence 8, Appli
11	574	35.9	1037	4	US-09-386-642-60	Sequence 60, Appl
12	526.5	32.9	1460	4	US-09-370-838-80	Sequence 80, Appl
13	526.5	32.9	1517	1	US-08-508-448C-15	Sequence 15, Appl
14	526.5	32.9	2790	4	US-09-370-838-79	Sequence 79, Appl
15	524.5	32.8	1462	4	US-09-370-838-55	Sequence 55, Appl
16	522.5	32.7	696	1	US-08-508-448C-24	Sequence 24, Appl
17	510.5	31.9	901	1	US-08-508-448C-9	Sequence 9, Appli
18	508	31.8	2479	3	US-09-342-749-29	Sequence 29, Appl
19	508	31.8	2479	4	US-09-691-840-29	Sequence 29, Appl
20	506	31.6	1479	3	US-09-342-749-1	Sequence 1, Appli
21	506	31.6	1479	4	US-09-691-840-1	Sequence 1, Appli
22	505.5	31.6	1615	4	US-09-820-002-1	Sequence 1, Appli
23	505.5	31.6	1783	4	US-09-510-738A-188	Sequence 188, App
24	505.5	31.6	1783	4	US-09-861-966-188	Sequence 188, App
25	502	31.4	2363	4	US-09-742-703-3	Sequence 3, Appli
26	497	31.1	2413	4	US-09-518-046-1	Sequence 1, Appli
27	497	31.1	1077	3	US-08-807-151-2	Sequence 2, Appli
28	491.5	30.7	1077	4	US-09-478-957-2	Sequence 2, Appli
29	482	30.1	1605	2	US-09-000-846-1	Sequence 1, Appli
30	478.5	29.9	959	4	US-09-023-942A-25	Sequence 25, Appl
31	473	29.6	2544	3	US-09-518-046-3	Sequence 3, Appli
32	456.5	28.5	2416	3	US-09-261-416-1	Sequence 1, Appli
33	455	28.4	1100	4	US-09-023-942A-5	Sequence 5, Appli
34	453.5	28.3	1613	4	US-09-387-375-1	Sequence 1, Appli
35	451.5	28.2	897	2	US-08-956-267A-1	Sequence 1, Appli
36	450.5	28.2	1081	4	US-09-008-271A-15	Sequence 15, Appl
37	444	27.8	1094	4	US-09-023-942A-3	Sequence 3, Appli
38	444	27.8	3147	2	US-09-027-337-1	Sequence 1, Appli
39	444	27.8	3147	4	US-09-644-600-1	Sequence 1, Appli
40 c	444	27.8	3147	4	US-09-644-600-18	Sequence 18, Appl
41	443.5	27.7	825	3	US-09-120-582-1	Sequence 1, Appli
42	442.5	27.7	980	4	US-09-023-942A-30	Sequence 30, Appl
43	442.5	27.7	1110	4	US-09-386-653A-1	Sequence 1, Appli
44	437.5	27.3	1212	4	US-09-620-312D-431	Sequence 431, App
45	431.5	27.0	1225	4	US-09-734-675-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-008-271A-18
; Sequence 18, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;   Hillman, Jennifer L.
;   Yue, Henry
;   Guegler, Karl J.
;   Corley, Neil C.
;   Tang, Tom Y.
;   Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Dr.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/008,271A
;   FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: <Unknown>
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Mohan-Peterson, Sheela
;   REGISTRATION NUMBER: 41,201
;   REFERENCE/DOCKET NUMBER: PF-0458 US

```
            TELECOMMUNICATION INFORMATION:
                  TELEPHONE: 650-855-0555
                  TELEFAX: 650-845-4166
      INFORMATION FOR SEQ ID NO: 18:
            SEQUENCE CHARACTERISTICS:
                  LENGTH: 2038 base pairs
                  TYPE: nucleic acid
                  STRANDEDNESS: single
                  TOPOLOGY: linear
            IMMEDIATE SOURCE:
                  LIBRARY: COLNNOT13
                  CLONE: 1337018
            SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-008-271A-18
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Alignment Scores:
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Pred. No.:              5.58e-130          Length:               2038
Score:                  1266.00            Matches:              228
Percent Similarity:     98.29%             Conservative:         2
Best Local Similarity:  97.44%             Mismatches:           4
Query Match:            79.12%             Indels:               0
DB:                                        Gaps:                 0
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US-09-607-745-9 (1-292) x US-09-008-271A-18 (1-2038)

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Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
            ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  803 CGTGTGGTGGGTGGGGAGGCCTCTGTGGAATTCTTGGCCTTGGCAGGTCAGCATCCAG 862

Qy   71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  863 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 922

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  923 GCCCACTGCTTCAGGAAACATACGATGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 982

Qy  111 LysLeuGlySerPheProSerLeuAlaValAlaValAlaLysIleIleIleIleGluAsnPro 130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  983 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1042

Qy  131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1043 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1102

Qy  151 GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro 170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1103 GGCACAGTGCAGGCCCATCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1162

Qy  171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysLysMetSerAspIleLeu 190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1163 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGAGGGAAGATGTCTGACATACTG 1222

Qy  191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrArgIle 210
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1223 CTGCAGGCGGTCAGTGCAGGTCATTGACAGCACACGGTGCAATGCAGCGATGCGTACCAG 1282

Qy  211 GlyGluValThrGluLysMetCysAlaGlyValIleProGluGlyGlyValAspThrCys 230
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1283 GGGGAAGTCACCGAGAAGATGTGTGCAGGGGTGATACCAGAAGGGGGTGTGGACACCTGC 1342

Qy  231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerArgAspGlnTrpHisValValGlyIle 250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1343 CAGGGTGACAGTGGTGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC 1402

Qy  251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1403 GTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1462

Qy  271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
            ||||||||||||||||||||||||||||||||||||||||||
Db 1463 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1504
```

RESULT 2
```
US-09-656-002-1
;   Sequence 1, Application US/09656002
;   Patent No. 6455668
;   GENERAL INFORMATION:
;      APPLICANT: Mack, David
;      APPLICANT: Gish, Kurt
;      APPLICANT: Wilson, Keith
;      TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AI
;      TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
;      FILE REFERENCE: A-69108/DJB/JUD/AMS
;      CURRENT APPLICATION NUMBER: US/09/656,002
;      CURRENT FILING DATE: 2000-09-06
;      PRIOR APPLICATION NUMBER: US 09/525,993
;      PRIOR FILING DATE: 2000-03-15
;      PRIOR APPLICATION NUMBER: US 09/493,444
;      PRIOR FILING DATE: 2000-01-28
;      PRIOR APPLICATION NUMBER: PCT/US 00/07044
;      PRIOR FILING DATE: 2000-03-15
;      NUMBER OF SEQ ID NOS: 3
;      SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 1
;      LENGTH: 2079
;      TYPE: DNA
;      ORGANISM: Homo sapiens
US-09-656-002-1
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Alignment Scores:
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Pred. No.:              5.74e-130          Length:               2079
Score:                  1266.00            Matches:              228
Percent Similarity:     98.29%             Conservative:         2
Best Local Similarity:  97.44%             Mismatches:           4
Query Match:            79.12%             Indels:               0
DB:                                        Gaps:                 0
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US-09-607-745-9 (1-292) x US-09-656-002-1 (1-2079)

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Qy   51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
            ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  818 CGTGTGGTGGGTGGGGAGGCCCTCTGTGGAATTCTTGGCCTTGGCAGGTCAGCATCCAG 877

Qy   71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  878 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 937

Qy   91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  938 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 997

Qy  111 LysLeuGlySerPheProSerLeuAlaValAlaValAlaLysIleIleIleIleGluAsnPro 130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  998 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC 1057

Qy  131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1058 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1117

Qy  151 GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro 170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1118 GGCACAGTGCAGGCCCATCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1177

Qy  171 LeuTrpIleIleGlyTrpGlyPheThrLysGlyGlyLysMetSerAspIleLeu 190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1178 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGAGGGAAGATGTCTGACATACTG 1237

Qy  191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrArgIle 210
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1238 CTGCAGGCGGTCAGTGCAGGTCATTGACAGCACACGGTGCAATGCAGCGATGCGTACCAG 1297

Qy  211 GlyGluValThrGluLysMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1298 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC 1357
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Qy  231  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1358 CAGGGTGACAGTGGTGGGGCCCCTGATGTACCAATCTGACCAGTGGCATGGTGGGGCATC 1417

Qy  251  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1418 GTTAGTTGGGGTATGGCTGCGGGGGCCCGAGCACCCCAGGGTATACACCAAGGTCTCA 1477

Qy  271  AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
         ||||||||||||||||||||||||||||||||||||||||||
Db  1478 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1519
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RESULT 3
US-09-387-375-8
; Sequence 8, Application US/09387375
; Patent No. 6485957
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/09/387,375
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-09-387-375-8

Alignment Scores:

Pred. No.:	4.45e-75	Length:	1130
Score:	765.00	Matches:	164
Percent Similarity:	62.93%	Conservative:	38
Best Local Similarity:	51.09%	Mismatches:	85
Query Match:	47.81%	Indels:	34
DB:		Gaps:	10

US-09-607-745-9 (1-292) x US-09-387-375-8 (1-1130)

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Qy  1    MetAspSerLysGlySerGlnLysSerArgLeuLeuLeuLeuLeuValValSerAsn 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13   ATGGACAGCAAAGGTTCGTCGCAGAAATCCCGCGTCCTGCTGCTGCTGGTGTCAAAT 72

Qy  21   LeuLeuLeuCysGlnGlyValValAlaSerAspTyrLysAspAspAspAlaAspAlaAla 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  73   CTACTCTTGTGCCAGGGTGTGGTCGCGAGCGACTACAAGGACGACGACGCGGACGCGGCC 132

Qy  41   AlaLeuAlaAlaProPheAspAspAspLysIleValGlyGlyTyrAlaLeuAspVal 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133  GCTCTTGCTGCCCCCTTTGATGATGATAAGATCGTTGGGGGCTATGCTCTAGAGGAC 192

Qy  61   AspSerTrpProTrpGlnValSerIleGlnTyrArgLysAspLysHisValCysGlyGlySer 80
         |||||||||||||||||||||||||||::::|||||||||||||||||||||||||
Db  193  GGAGAGTGGCCGTGGCAGGTCAGCATCCAGCATCCTGGGCACCGTGTGCGGGGGTCG 252

Qy  81   IleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAspVal 100
         |||||||||||||||||||||||||||||||::::|||::|||
Db  253  CTCATCGACCCCCAGTGGGTGCTGACAGCCGCGCACTGCTTCCCAGAGGGGCACTGCCA 312

Qy  101  PheAsnTrpLysValArgAlaGlySerAspLysGlySerPhePro----------- 116
         ||||||:::|||||::|||||:: :::|||||||
Db  313  GCTGAGTACCGGCGCCGCGGGGCGGCTCCACCTGGCTCCGGCTC 372

Qy  117  SerLeuAlaValAlaLysIleIleIleIlePheAsnProMetTyrProLysAsp--- 135
         |||:||  :::|||||:::||||
Db  373  TCGGTGCCCGTGCCAGCGGGGCTGCTG------CCCCCGGACTACTCCGAGGACGCGGG 423
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Qy  136  -----AsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrVal 153
              :::::||:::|||||||||:::::|||::: :||
Db  424  GCCCGGCCGGCGACCTGCTGCACTGCTGCAGCTGGCGGTCGCCGTGCCCGTGCGCGGTC 483

Qy  154  ArgProIleCysLeuProPhePheAspGluGluThrProAlaThrProLeuTrpIle 173
         :::||||:||:|||||||||||||||
Db  484  CAACCCGTCGCTGCCTGCCGTGCCGCGGCCGCCGCCCGGCCACCATGCCGGGTC 543

Qy  174  IleGlyTrpGlyPheThrLysGlnGlnAsnGlyGlyLysMetSerAsp-----IleLeuLeu 191
         ||||||||||:||  ||  ::: :::
Db  544  ACCGGCTGGGGC--AGCCTCCGGCCAGAGAGTGCCCTCCAGAGGTGGACCGGCTACAA 600

Qy  192  GlnAlaSerValGlnValIleAspSerThrArgCysAsn------AlaAsp 206
                   :::::|||:||::: :||:
Db  601  GGAGTAAGGTGCCCGCTGCTGACTCGCGCACCTGCGACGGGCCTCTACCAGTGGGCGCG 660

Qy  207  AspAlaTyrGlnGlyGlu------ValThrGluLysMetCysAlaGlyIleProGlu 224
         |||         :::||||||||
Db  661  GACGTGCCCCAGGCTGAGCGACGCATTGTGCTGCCTGGGAGTCTGTGTGGCGGCTACCCCAG 720

Qy  225  GlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeu--MetTyrGlnSerAsp 243
         |||  |||:|||||:||||||:|||||||||||:  :|||:||
Db  721  GGCCACAAGGACGCGCCTGGCCAGGGTGATTCTGGGGGACCCTGACCTGCCTGCCAGTCTGGG 780

Qy  244  GlnTrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrPro 263
         |||   :::|||:|||:::|||:|||||||||:::|||
Db  781  AGCTGGGTCCTGGTGGGCGTGGGTGGAGCGTGGGCAAGGGTTGTGCCTGCGCCCAACCGTCCA 840

Qy  264  GlyValTyrThrLysValSerAlaTyrLeuAsnTrpIle 276
         ||||||||||:::|:|:|||:::|||
Db  841  GGGGTCTACACCAGTGTGCCACATATAGCCCTGGATTCAGGCTGCCGTCACTTCTAAT 900

Qy  277  ------------TyrAsnValTrpLysAlaGluLeuSerArgHisHisHisHis 291
                     ||||:::||
Db  901  GCTTCTAGATACCCCTACGATGTG---CCCGATTACGCGCCGTAGACATCACCATCACCAT 957

Qy  292  His 292
         |||
Db  958  CAC 960
```

RESULT 4
US-09-386-653A-8
; Sequence 8, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
; OTHER INFORMATION: Protease T in a zymogen activation vector
US-09-386-653A-8

Alignment Scores:

Pred. No.:	6.41e-74	Length:	1130
Score:	754.50	Matches:	156
Percent Similarity:	62.73%	Conservative:	46
Best Local Similarity:	48.45%	Mismatches:	83
Query Match:	47.16%	Indels:	37
DB:		Gaps:	10

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; Patent No. 6420157
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Zymogen Activation System
;  FILE REFERENCE: ORT-1028
;  CURRENT APPLICATION NUMBER: US/09/386,642
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;  LENGTH: 1169
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;  OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-7

  Alignment Scores:
  Pred. No.:
  Score:                    5.83e-73           Length:            1169
                            746.00             Matches:           163
  Percent Similarity:       60.37%             Conservative:      35
  Best Local Similarity:    49.70%             Mismatches:        94
  Query Match:              46.62%             Indels:            36
  DB:                                          Gaps:              8

US-09-607-745-9 (1-292) x US-09-386-642-7 (1-1169)

Qy    1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13 ATGGACAGCAGAAAGGTTCGTCGCAGAGAAATCCCGCCTGCTGCTGGTGTGTCAAAT  72

Qy   21 LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspAspAspValAspAlaAla  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   73 CTACTCTTGTGCCAGGGTGTGTCCGACTACAAGGACGACGACGACGTGGACGCGGCC 132

Qy   41 AlaLeuAlaAlaProPheAspAspAspLysIleValGlyGlyTyrAlaLeuAspPheVal  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133 GCTCTTGCTGCCCCCTTTGATGATGACAAGATCGTTGGGGGTTATGCTCTAGAGGCC 192

Qy   61 AspSerTrpProTrpGlnValSerIleGlnTyrAspLysHisValCysGlyGlySer  80
         |||:::  |||||||||||||||||:::  ||||||
Db  193 GGCGAGTGGCCCTGGCAAGTCAGCATCCAGCGCAACGGAAGCCACTTCTGCGGGGCAGC 252

Qy   81 IleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAspVal 100
         :::::|||
Db  253 CTCGTGTCTGAGCCAGTGGGTGCTGTCAGCTGCTTCCCCAGCGAGCACCACAAG 312

Qy  101 PheAsnTrpLysValArgAlaGlySerLeuGlySerPheProSerLeuLeuAla--- 119
         :::::||||||||
Db  313 GAAGCCTATGAGCTCAAGCTGGGGCGCCCACCAGCTCCTACTCCAGGACGCCAAG 372

Qy  120 ValAlaLysIleIleIleIleGluPheAsnProMetTyrProLysAsp------Asn 136
         ::  :::  ||
Db  373 GTCAGCACCCTGAAGGACATCATCCCCACCAGTACCTACCCTGGGAGGGTCCCAGGGC 432

Qy  137 AspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIle 156
         :::::|||||
Db  433 GACGTGCTGGCCCTGAGCTGGTGCTCAGAGCCCATCCGAGGCCAACTCACCTTCTCAGCTGC 492

Qy  157 CysLeuProPhePheAspGluLeuThrProAlaThrProLeuTrpProLeuGlyTrp 176
         ::  |||||
Db  493 TGCCTCCCTGCACCAACGCCCCAGTCCTGGGTGACAGGCTGGGCTCCCAGGGC 552

Qy  177 GlyPheThrLysGlnAsnGlyGlyLysMetSer---AspIleLeuLeuGlnAlaSerVal 195
         |||  :::::::
Db  553 GGTCATGTGGCCCCTCGGCCCTCTGACGCCCAAGCGCCTGAGCAACTCGAGGTG 612

Qy  196 GlnValIleAspSerThrArgCysAsnAla--------AspAspAlaTyrGlnGlyGlu 212
         ::::|||
Db  613 CCTCTGATCAGTCGTGAGACGTGTAACTGCCTGTACAACATCGAGCTACAAGCCTCAAGCCTGAGGAG 672
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RESULT 5
US-09-386-642-7
; Sequence 7, Application US/0938642

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US-09-607-745-9 (1-292) x US-09-386-653A-8 (1-1130)

Qy    1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13 ATGGACAGCAGAAAGGTTCGTCGCAGAGAAATCCCGCCTGCTGCTGGTGTGTCAAAT  72

Qy   21 LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspAspAspValAspAlaAla  40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   73 CTACTCTTGTGCCAGGGTGTGTCCGACTACAAGGACGACGACGACGTGGACGCGGCC 132

Qy   41 AlaLeuAlaAlaProPheAspAspAspLysIleValGlyGlyTyrAlaLeuAspPheVal  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133 GCTCTTGCTGCCCCCTTTGATGATGACAAGATCGTTGGGGGTTATGCTCTAGAGGAG 192

Qy   61 AspSerTrpProTrpGlnValSerIleGlnTyrAspLysHisValCysGlyGlySer  80
         |||:::
Db  193 GGCGAGTGGCCCTGGCAAGTCAGCATCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGC 252

Qy   81 IleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAspVal 100
         :::::
Db  253 CTCATCGCCGACGCCAGTGGTCCTGACGGTGCTGCGCGACCACACCTCTGAGACG 312

Qy  101 PheAsnTrpLysValArgAlaGlySerLeuGlySerPheProSerLeuLeuAla--- 119
         :::::  :::|||
Db  313 TCCCTGTACAGGTCCTGCTGGGGCAAGGCAGTCGAGTGCAGCGGGACCACAGCTATG 372

Qy  120 ValAlaLysIleIleIleIleGluPheAsnProMetTyr-------ProLysAspAsn 136
         :::||
Db  373 TATGTCCCGGGTGAGGCAGTGGAGAGCAACCACCCCCTGTACCAGGGCCACGGCCTCCAGCGCT 432

Qy  137 AspIleAlaLeuMetLysLeuGlnPheProSerGlyThrPheSerGlyThrValArgProIle 156
         :::::||||||
Db  433 GACGTGCTGGCCCTGTGGAGCTGGAGCGGCACCAGTGCCCTTCACCAATTACCTCCCCGTG 492

Qy  157 CysLeuProPhePheAspGluLeuThrProAlaThrProLeu-----TrpProIleIle 174
         :::
Db  493 TGCCTGCCT------GACCCCCTCGGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACT 546

Qy  175 GlyTrpGlyGlyValPheThrLysGlnAsnGlyGlyLysLysMetSerAsp-------- 188
         :::|||
Db  547 GGCTGGGGCAGCCAGGTGAG--------GAAGACCTCGCCCGAACCGCGG 591

Qy  189 IleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsn--------- 204
         :::::
Db  592 ATCCTGCAGAAACTCCTGTGCCCATCATCGACACACACCAAGTGCAACCTGCTCTACAGC 651

Qy  205 -----AlaAspAspAlaTyrGlnGlyGlu---ValThrGluLysLysMetCysAlaGly 221
         :::
Db  652 AAAGACACCAGTTTGGCTACCAACCCAAACCATCAAGAATGACAATGACAATGTGCGCCGGC 711

Qy  222 IleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln 241
         :::|||
Db  712 TTCGGAGAGGGCAGAAGAAGGATGCTGCGAAGGGGACTCGGGGCGCCCCCGTGGTGCCTC 771

Qy  242 SerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrCysGlyGlyPro 260
         ::  |||||
Db  772 GTGGGTCAGTCGTGCGTGCAGGCGGGGTGATCAGTCGGGGTGAGGGCTTGGGGCTCCCAGGAG 831

Qy  261 SerThrProGlyValTyrThrLysValTyrLeuAsnTrpIleTyrAsnVal---- 279
         :::::|||
Db  832 AACCGCCCCAGGTGTCTACATCCGTCCACGGCCCCACCACCTGCTGGGTCACTCCGGATCATC 891

Qy  280 -------------TrpLysAlaGluLeuSerArgHisHisHisHis 290
         ::  |||||
Db  892 CCAAACTGCAGTTCCAGCCAACGGCCTCCTTCCCCAACGGGCCTCCAGAAGCTGTCTAGACATCACCACCATCAC 951

Qy  291 HisHis 292
         |||||
Db  952 CATCAC 957
```

```
Qy  213 ------ValThrGluLysMetMetCysAlaGlyTyrIleProGluGlyGlyValAspThr 229
                 |||||||     :::||||    ||||||||
Db  673 CCGCACTTTGTCCAAGAGAGGAGGAGGTGTGTGCTGGCTATGTGAGAGGGGGCAAGAGACGCC 732

Qy  230 CysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAsp---GlnTrpHisValVal 248
                 ::     |||||||||:::||
Db  733 TGCCAGGGTGACTCTGGGGGCCACTCTGCCCGTGGGAGGGTCTCTGGTACCTGACG 792

Qy  249 GlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLys 268
                 ||||||||||||||     |||||     |||:::
Db  793 GGCATTGTGAGCTGGGGAGATGCCTGTGGGCCCCAACAGGCCTGGTGTGTACACTCTG 852

Qy  269 ValSerAlaTyrLeuAsnTrpIleTyr------ 277
                 ::||||||||||:::
Db  853 GCCTCCAGCTATGCCTCCTGGATCCAAAGCAAGGTGACAGAACTCCAGCTCGTGTGGTG 912

Qy  278 ------AsnValTrpLysAlaGluLeu--- 284
                 |||:::  :::
Db  913 CCCAAACCCAGGAGTCCCGACAACCTCTGTGGCAGCCACCTGGCCTTCAGC 972

Qy  285 SerArgHisHisHisHisHis 292
                 |||||||||||||||||||||
Db  973 TCTAGACATCACCATCACCATCAC 996
```

RESULT 6
US-09-386-629-2
; Sequence 2, Application US/09386629
; Patent No. 6426199
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L.
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Idenification and Characterization of the complementary
; TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
; FILE REFERENCE: ORT-1030
; CURRENT APPLICATION NUMBER: US/09/386,629
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1166
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
; OTHER INFORMATION: domain in a zymogen activated construct
US-09-386-629-2

Alignment Scores:

Pred. No.:	2.35e-72	Length:	1166
Score:	740.50	Matches:	164
Percent Similarity:	61.70%	Conservative:	39
Best Local Similarity:	49.85%	Mismatches:	87
Query Match:	46.28%	Indels:	39
DB:	4	Gaps:	10

US-09-607-745-9 (1-292) x US-09-386-629-2 (1-1166)

```
Qy    1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn 20
                 |||   |||
Db   13 ATGGACAGCAAAGGTTCGTCGCAGAAATCCCGCCTGCTCCTGCTGGTGGTGTCAAAT 72

Qy   21 LeuLeuLeuCysGlnGlyValValValSerAspTyrLysAspAspAspAspValAlaAspAlaAla 40
                 ||||||:::  |||||||||
Db   73 CTACTCTTGTGCCAGGGTGTGTTCTCGACTACAAGGACGACGACGACGTGGACGCGGCC 132

Qy   41 AlaLeuAlaAlaProPheAspAspAspAspLysIleValGlyGlyTyrAlaLeuAspVal 60
                 |||         |||||||
Db  133 GCTCTTGCTGCCCCCTTTGATGATGACAAGATCGTTGGGGGCTATGCTCTAGAGGAC 192

Qy   61 AspSerTrpTrpProGlnValSerIleGlnTyrAspArgSerGlnHisValCysGlyGlySer 80
                 :::   |||  |||||||
```

RESULT 7
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 10
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```
Db  193 AGGCGAGTGGCCCTGGATCGTGAGCATCCAGAAGAATGGGACCCACCTGCGCAGGTTCT 252

Qy   81 IleLeuAspProHisTrpValThrAlaAlaHisCysPheArgLysHisThrAsp--- 99
                 :::|||  :::  ::
Db  253 CTGCTCCACCAGCCGCTGGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAA 312

Qy  100 ValPheAsnTrpLysValArgAlaGlyLeuGlySerPheProSerLeuAla 119
                 ||||||||||||     ::||
Db  313 CCATACCTGTTCTCTGTGTCGTGCTGGGCCTGGGCAGCTGGGGAAC--CCTGGCCTCTCGG 369

Qy  120 ValAlaLysIleIle------IleGluPheAsnProMetTyrPro--LysAspAsn 136
                 ||:::    ::::
Db  370 TCCCAGAAGTGGGTGTTGCCTGGTGAGCGCCACCCTGTTATTCCTGGAAGGAAGGT 429

Qy  137 ------AspIleAlaLeuMetLysGlnPheProLeuThrPheSerGlyThrVal 153
                 ||||:::::::  :::
Db  430 GCCTGTGCAGACATTGCCTGGTGCTCCATACAGTTCTCAGAGCGGGTC 489

Qy  154 ArgProIleCysLeuProPheAspGluLeuThrProAlaThrProLeuTrpIle 173
                 |||||||     |:::||
Db  490 CTGCCCATCTGCCTACCTGATGCTCTATCCACCTCCCTCCAAACACCCACTGTGGATC 549

Qy  174 IleGlyTyrPheThrLysGlnAsnGlyGlyLysMet------SerAspIleLeuLeu 191
                 |||  ::  ||
Db  550 TCAGGCTGGGGG--AGCATCCAAGATGGAGTTCCCTTGCCCACCCTCAGACCCTGCAG 606

Qy  192 GlnAlaSerValGlnValIleAspSerThrArgCysAsnAla------AspAspAla 208
                 |||    :::||
Db  607 AAGCTGAAGGTTCCTATCATCGACTCGGAAGTCTGCGAGCCATCTGTACTGGCGGGAGCA 666

Qy  209 TyrGlnGlyAspValThrGluLysMetMetCysAlaGlyLeuIleProGluGlyGlyValAsp 228
                 :::|||||||||||||||:::  ||||||
Db  667 GGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTTGAGGGGGAGCGGGAT 726

Qy  229 ThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAsp--GlnTrpHisVal 247
                 ||||||||||||||||     |||    :::
Db  727 GCTTGTCTGGGGACTCCGGGGGCCCTCATGTGCCAGGTGGACGGGCCTGCTGCTG 786

Qy  248 ValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThr 267
                 ||||||||||||||     |||
Db  787 GCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGGCGCCACAGGCCCGGGGTCTACATC 846

Qy  268 LysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrpLys------ 281
                 :::||||||||  :::  ::
Db  847 AGCCTCTCGCCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTCCAGCTCCGCGGG 906

Qy  282 ------AlaGlu 283
                 |||
Db  907 CGCGCTCAGGGGGTGGGCCCTCAGGGCACCAGGCCAGGCTCTGGGCGCCGCCGCGGC 966

Qy  284 LeuSerArgHisHisHisHisHis 292
                 ||||||||||||||||||||
Db  967 TCCTCTAGACATCACCATCACCATCAC 993
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

Alignment Scores:
Pred. No.:                           1052
Score:            6.43e-65           Matches:                148
Percent Similarity:   61.31%         Conservative:            39
Best Local Similarity:  48.52%       Mismatches:              89
Query Match:          42.03%         Indels:                  29
DB:                                  Gaps:                    11

US-09-607-745-9 (1-292) x US-09-386-642-10 (1-1052)

Qy      1  MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn    20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13  ATGGACAGCAAAGGTTCGTCGCAGAAATCCCGCCTGCTCCTGCTGGTGGTGTCAAAT    72

Qy     21  LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspAspValAspAlaAla    40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73  CTACTCTGTGCCAAGGTGTGGTCTCCGACTACAAGGACGACGACGTGGACGCGGCC    132

Qy     41  AlaLeuAlaAlaProAspAspAspAspLysIleValGlyGlyTyr---AlaLeuAsp    59
           ||||||||||||            ::|||||||||||||           |||:::
Db    133  GCTCTTGCTGCCCCCTTTGATGATGATGACAAGATCGTTGGGGGCTACAACTGTCAAGAA    192

Qy     60  ValAspSerTrpProTrpGlnValSerIleGlnTyrArgLysValCysGlyGly    79
           ||:||||||||||||||||||||||||||||||||||:    ::  :
Db    193  AAGCACTCCCAGCCCTGGGCAGGCAGGGCTACTGTGTGGGGCG    252

Qy     80  SerIleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLys------    96
           ::|||||||||||::||||||||||||||::
Db    253  ACGCTCATCGCCCCAGATGGCTCTGACAGCAGCCCACTGCCTCCAAGCCCGTACATA    312

Qy     97  ---HisThrAspValPheAsnValTrpArgAlaGlySerAspLys-----------   111
           |||          :::                   :::::
Db    313  GTTCACCTGGGGCAGGCAGCAACCTCCAGAAGGAGGAGGGTGTGAGCAGACCCGGACAGCC    372

Qy    112  LeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluProAsnProMet   131
           ||||||||          :::||||||
Db    373  ACTGAGTTCCTTCCCCCACCCCGGC---------------------TTCAACAACAGC    408

Qy    132  TyrPro------LysAsp-----AsnAspIleAlaLeuMetLysLeuGlnPheProLeuThr   148
           |||          :::          ::||||||||||||||::::
Db    409  CTCCCCAACAAAGACCACCGCAATGGCATGCTGGTGAAGATGGCATCGCCAGTCTCC    468

Qy    149  PheSerGlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAla   168
           ||||||||||          ::  ||||||||:::
Db    469  ATCACCTGGCTGTGCGACCCCTCACCCTCC-----TCACGCTGTGTCACTGCTGGC    522

Qy    169  ThrProLeuTrpIleIleGluTyrThrGlyPheThrLysGlnAsnGlyAlaGlyLysMetSerAsp   188
           ||||||||||          :::::
Db    523  ACCAGGTGGCTGCCTCATTTCCGGCTGGGGCAGCCCCCAGTTACGCCTGCCTCAC    582

Qy    189  IleIleLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAla   208
           |||||||||||          :: :::
Db    583  ACCTTGCGATGCGCCAACATCACCATCATTGAGCACGAAGTG-----GAGACGCC    636

Qy    209  TyrGlnGlyValThrGluGluProLysLysMetMetCysValAlaGlyTyrLeuProGlyGlyIleValAsp   228
           ||||||||||          :::::
Db    637  TACCCCGGCAACATCACCAGACCAGACATCACAGAGAAGGGGCAAGGAC    696

Qy    229  ThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValTyrTrpHisValVal   248
           ||||||||||          :::||||
Db    697  TCCTGCCAGGGTGACTCCGGGGGCCCCTGTCTGTAACCAGTCT-------CTTCAA    747

Qy    249  GlyIleValSerAlaTyrLeuTyrArgGly--CysGlyGlyProSerThrGlyProValTyrThr   267
           ||||||||||          :::||||||
Db    748  GGCATTATCTCCGGGGCCAGGATCCGGTGCGATACCGGAAAGCCTGGTGTCTACACG    807

Qy    268  LysValSerAlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeuSerArgHis   287
           ||||||||||          :::::
Db    808  AAAGTCTGCAAATATGTGGACTGGATCTACAGGAACGTGGTTCAAGCCCATGCAGC---TCTAGACAT    864
```

```
Qy    288  HisHisHisHisHis   292
           :||
Db    865  CACCACCACCATCAC   879
```

```
RESULT 8
US-09-386-642-9
; Sequence 9, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;   OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-9

Alignment Scores:
Pred. No.:                           1049
Score:            6.92e-62           Matches:                146
Percent Similarity:   60.33%         Conservative:            38
Best Local Similarity:  47.87%       Mismatches:              91
Query Match:          40.31%         Indels:                  30
DB:                                  Gaps:                    11

US-09-386-642-9 (1-292) x US-09-386-642-9 (1-1049)

Qy      1  MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn    20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13  ATGGACAGCAAAGGTTCGTCGCAGAAATCCCGCCTGCTCCTGCTGGTGGTGTCAAAT    72

Qy     21  LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspAspValAspAlaAla    40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73  CTACTCTGTGCCAAGGTGTGGTCTCCGACTACAAGGACGACGACGTGGACGCGGCC    132

Qy     41  AlaLeuAlaAlaProPheAspAspAspLysIleValGlyGlyTyr---AlaLeuAsp    59
           ||||||||||            ::|||||||||||||           |||:::
Db    133  GCTCTTGCTGCCCCCTTTGATGATGATGACAAGATCGTTGGGGGCTACAACTGTCTAGAA    192

Qy     60  ValAspSerTrpProTrpGlnValSerIleGlnTyrArgLysValCysGlyGly    79
           ||:||||||||||||||||||||||||||||||||||:    ::  :
Db    193  CCCCATTCGCAGCCTTGGCAGGCAGGGCCAGCAACTACTCTGTGCCGGGT    252

Qy     80  SerIleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArg------LysHisThr    98
           ::|||||||||||::||||||||||||||::
Db    253  GTCCTTGTAGGTCGCAACTGGGTCTTCTTACAGCGTGCCCACTGTAAAAAACCGAAATACACA    312

Qy     99  AspValPheAsnTrpLysValArgAlaGlySerAspLeu-------------GlySer   114
           |||          :::                   :::::
Db    313  --------------------GTACGCCTGGGAGGACCACCAGCCTTCAGAAATAAAGATGGCCCA    354

Qy    115  PheProSerLeuAlaValAlaLysIleIleIleIleGluProAsnProMetTyr------   132
           ||||||||          :::||||||
Db    355  GAGCAAGAAATACCTGTGGTTCAGTCCATCCCA--------CACCCCTGCTACAACAGC    405

Qy    133  ---------ProLysAspAspAsnAspIleAlaLeuMetLysLysLeuGlnPheProLeuThr   148
           |||          :::          ::||||||||||::||
Db    406  AGCGATGTGGAGGACCACCAACCATGATCTGATGCTTCTTCAACTGCTGGTCAGGATCC    465

Qy    149  PheSerGlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAla   168
           ||||||||          ::  ||||||||:::
Db    466  CTGGGGTCCAAGTGAAGCCCATCAGCCTGCA-----GATCATTGCACCCAGCCCTGGC    519
```

```
Db  187  AGCCTGCGCCTGTGGGATTCCCACGTATGGGAGGTGAGGTGCTGCTCAGCCACCGTGGGCA  246

Qy   88  LeuThrAlaAlaHisCysPheArgLysThrAspValPheAsn----------TrpLys  104
         |||                                  :::  : ::         |||
Db  247  CTCACGGCGGCGCCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCTCCGGGTGGATG  306

Qy  105  ValArgAlaGlySerAspLysLeuGlySerPheProSerLeuAlaValAlaLys------  122
         ||| |                                  ::|:||
Db  307  GTCCAGTTGGC-----CAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTAC  360

Qy  123  ----------IleIleIleIleGluPheAsnProMetTyrProLysAspAsn--  136
                :::          ||:                   ::|:||
Db  361  TACAACCGTACTTGTATCGAATATCATCTGAGCCCTCGCTACCTGGGAATTCACCC  420

Qy  137  --AspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArgPro  155
         ||||||||     :::::::::                :||:||
Db  421  TATGACATTGCCCTTGGTGAAGCTGTCCACCTACACTAAACACATCGAGCCC  480

Qy  156  IleCysLeuProPhePheAspGluLeuThrProAlaThrProLeuTrpIleIleGly  175
         |||||||                  :|:|||
Db  481  ATCTGTCTCCAGCCTCCACATTGAGTTTGAGAACCGGACAGACTGTGGGTGACTGGC  540

Qy  176  TrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeuLeuGln--AlaSer  194
         |||||||                                              ||||||
Db  541  TGGGGGTACATCAAGAAGGATGAGCACTGCCATCTCCCACACCCTCCAGGAAGTTCAG  600

Qy  195  ValGlnValIleAspSerThrArgCysAsn-------AlaAspAspAlaTyrGlnGlyGly  211
         |||                  :::            AlaAspAspAlaTyrGlnGlyGly
Db  601  GTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTCCGCAAG  660

Qy  212  GluValThrGlyIleLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCysGln  231
         :::::                            :|||||
Db  661  GACATCTTGGAGACATGGTTTGCTGGCAATGCCCAAGGCGGGAAGGATGGCTGCTTC  720

Qy  232  GlyAspSerGlyGlyProLeu--MetTyrGlnSerAspGlnTrpHisValValGlyIle  250
         :::::                                 :|:|||
Db  721  GGTGACTCAGGTGGACCCCTGGCCTGTAACAAGAATGGACGTGGTATCAGATTGGAGTC  780

Qy  251  ValSerTrpGlyTyrGlyCysGlyProSerThrProGlyValTyrThrLysValSer  270
         |||                  :::
Db  781  GTGAGCTGGGGAGTGGGCTGTGGTCGGCCCCAATCGGCCCGGTGTCTCACCAATATCAGC  840

Qy  271  AlaTyrLeuAsnTrpIleTyrArgAsnVal----------------------  279
         ||||||
Db  841  CACCACTTTGAGTGGATCCAGAAGTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCC  900

Qy  280  ---TrpLysAlaGluLeuSerArgHisHisHisHis  292
            |||
Db  901  TCCTGG----------TCTAGACATCACCATCACCATCAC  930
```

RESULT 10
US-09-386-642-8
; Sequence 8, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-8

```
Qy  169  ThrProLeuTrpIleIleGlyTyrTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAsp  188
         :::                                                      ||||||
Db  520  CAGAAGTGCACCGTCTCAGGCTGGGGCCACTGTCACCGTCCCGGAGAGAATTTTCCTGAC  579

Qy  189  IleLeuLeuGlnAlaSerValGlnValIleAspThrArgCysAsnAlaAspAspAla  208
         ::::::                                  ::|:||
Db  580  ACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAGAAGTGT-----GAGGATGCT  633

Qy  209  TyrGlnIleGlyGluGluLysMetMetCysMetAlaGlyIleProGluGlyGlyValAspAsp  228
         ::::::                            ||:||||
Db  634  TACCCCGGGCAGATCACAGATGCCATGGTCTGTGCAGGCAGCAGCAAA--GGGGCTGAC  690

Qy  229  ThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnSerGlnTrpHisValVal  248
         :::::::                                   :|:|||
Db  691  ACGTGCCAGGGCGATTCTGGAGGCCCCCTGATGTGTGTGATGGT-------GCACTCCAG  741

Qy  249  GlyIleValSerTrpGlyTyrGly--CysGlyProSerThrProGlyValTyrThr  267
         |||||||                                   :|:|||
Db  742  GGCATCACATCCTGGGGCTCCAGACCCTGTGGAGGTCCGACAAACCTGGCGTCTATACC  801

Qy  268  LysValSerAlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeuSerArgHis  287
         :::                                   ::|:||
Db  802  AACACTCTGCGCTACCTGGATCGGGATCAAGAAGATCATAGGCAGCAAGGGCTCTAGACAT  861

Qy  288  HisHisHisHisHis  292
         |||||||||||||||
Db  862  CACCACCACCATCAC  876
```

RESULT 9
US-09-386-642-59
; Sequence 59, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1103
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence of human protease F in CFEK2 zymogen
; OTHER INFORMATION: vector
US-09-386-642-59

Alignment Scores:
Pred. No.:
Score: 4.67e-57
Percent Similarity: 58.50%
Best Local Similarity: 42.86%
Query Match: 37.59%
DB:

Length: 1103
Matches: 601.50
Conservative: 46
Mismatches: 85
Indels: 37
Gaps: 10

US-09-607-745-9 (1-292) x US-09-386-642-59 (1-1103)

```
Qy   28  ValSerAspTyrLysAspAspAspAspLysValAspAlaAlaAlaAlaLeuAlaAlaProPheAsp  47
         |||||||                                               |||||||
Db   73  GTCCCCGACTACAAGGACGACGAC-----GACGGCGGCGCCGCTTCTTGCTGCCCCCCTTGAT  126

Qy   48  AspAspAspLysIleLeuValGlyGlyTyrAlaLeuAspValAspAspValAspSerTrpProTrpGlnVal  67
         |||||||                                               ::::::
Db  127  GATGATGACAAGATCGTTGGGGGCTATGCTCTAGAACTCGGGCGTTGGCCGTGGCAGGGG  186

Qy   68  SerIleGlnTyrAspLysGlnHisValCysGlyGlySerIleGluAspProHisTrpVal  87
         |||||||                            ::::::
```

```
Alignment Scores:
Pred. No.:                          Length:            1142
Score:              4.25e-56        Matches:           133
Percent Similarity: 55.81%          Conservative:      35
Best Local Similarity: 44.19%       Mismatches:        95
Query Match:        37.06%          Indels:            38
DB:                                 Gaps:              9

US-09-607-745-9 (1-292) x US-09-386-642-8 (1-1142)

Qy   28  ValSerAspTyrLysAspAspAspValAspAlaAlaAlaLeuAlaAlaProPheAsp  47
         ||||:||                                    ||||:||
Db   73  GTCCCGACTACAAGGACGACGAC------GACGCGGCCCTCTTGCTGCCCCCTTTGAT  126

Qy   48  AspAspAspLysIleValGlyGlyTyrAlaLeuAspSerTrpProTrpGlnVal  67
         |||||||||:||||||||||||:||
Db  127  GATGATGACAAGATCGTTGGGGGCTATGCTCTAGAGGCCGGTCAGTGCCCTGGCAGGTC  186

Qy   68  SerIleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpVal  87
         ||||||:|||||:
Db  187  AGCATCACCTATGAAGGCCTCCATGTGTGGTGGTCTCTCGTGTCTGAGCAGTGGGTG  246

Qy   88  LeuThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAla  107
         :::::|||:::
Db  247  CTGTCAGCTGCTCACTGCTTCCCCAGCGACACCACAAGCAGAAGCTATGAGGTCAAGCTG  306

Qy  108  GlySerAspLysLeuGlyGlySerPheProSerLeuAla--ValAlaLysIleIleIleIle  126
         ||:|||:||||                              ||||||||||||||
Db  307  GGGGGCCCACCAGCTAGACTCCTACTCCGAGGACGGTCAAGGTCAGCACCCTGAAGGACATC  366

Qy  127  GluPheAsnProMetTyrProLysAsp-------AsnAspIleAlaLeuMetLysLeu  143
         :::||:::|:                       |||:||
Db  367  ATCCCCCACCCCAGCTACCTCCAGGAGGGCTCCCAGGGGCCGACATTGCACTCCTCCAACTC  426

Qy  144  GlnPhePheProLeuThrPheSerGlyThrValArgProIleCysLeuProPheAspGlu  163
         ||||||:::                                    ::
Db  427  AGCAGACCCATCACCTTCTCCGGCACACTCCGCCTACCTCCGGCCTCCCGCCAGCCAACCGCC  486

Qy  164  GluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGly  183
         ||||                                               :::
Db  487  TCCTTCCCACGGCCTTCCACTGGCACTGCTGGGTCATGTGGCCCCTCAGTG  546

Qy  184  GlyLysMetSer---AspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg  202
         ||:|||                                                 |||||
Db  547  AGCCTCCTGACGCGCCCAAGCCACTGCAGCAACTCGAGGTGCCTCGATCAGTCGTGAGACG  606

Qy  203  CysAsnAla--------AspAspAlaTyrGlnGlyGlu------ValThrGluLys  216
         ||||                                             |||||||
Db  607  TGTAACTGCCTGTACAACATCGACGCCAAGCCTGAGGAGCCCACTTTGTCCAAGAGGAC  666

Qy  217  MetMetCysSerAlaGlyIleProGluGlyIleGlyValAspThrCysGlnGlyAspSerGlyGly  236
         |||||||||||||||||||||||||||||||||||||||||
Db  667  ATGGTGTGTGGGCTATGTGGAGGGGGCAAGAGCGTGACTCTGGGGGC  726

Qy  237  ProLeuMetTyrGlnSerAsp--GlnTrpHisValValGlyIleValSerTrpGlyTyr  255
         :::                   |||:::||
Db  727  CCACTCTCCTGCCCTGTGGAGGTCTCTGGTACCTGACGGGCATTGTGAGCTGGGGAGAT  786

Qy  256  GlyCysGlyGlyProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrp  275
         ||||                                               :::::
Db  787  GCCTGTGGGGGCCCCGCAACAGGCCTGGTGTACACTCTGGGCCTCCAGCTATGCCTCCTGG  846

Qy  276  IleTyr-----  277
         |||
Db  847  ATCTACAAGCAGGTGACAGAACTCCAGCTGCCCCAAACCCAGGAGTCCCAG  906

Qy  278  -------AsnValTrpLysAlaGluLeu-------SerArgHisHisHisHis  291
                |||:::                    ||||||||||||
Db  907  CCCGACACCTCTGTGGCAGCCACCTGGCCTTAGCTGCCGACATCACCATCACCAT  966

Qy  292  His  292
         |||
Db  967  CAC  969
```

```
RESULT 11
US-09-386-642-60
; Sequence 60, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
;   OTHER INFORMATION: sequence of human MH2 protease in PFEK zymogen
;   OTHER INFORMATION: vector
US-09-386-642-60

Alignment Scores:
Pred. No.:                          Length:            1037
Score:              4.63e-54        Matches:           133
Percent Similarity: 57.14%          Conservative:      39
Best Local Similarity: 44.19%       Mismatches:        103
Query Match:        35.88%          Indels:            26
DB:                                 Gaps:              11

US-09-607-745-9 (1-292) x US-09-386-642-60 (1-1037)

Qy    1  MetAspSerLysGlySerGlnLysSerArgLeuLeuLeuValValSerAsn  20
         |||||
Db   13  ATGGACAGCAAAGGTTCGTCGCAGAAATCCCGCGCTCCTGCTGGTGGTGTCAAAT  72

Qy   21  LeuLeuLeuCysGlnGlyValValValSerAspTyrLysAspAspAspValAspAlaAla  40
         |||||                              :::
Db   73  CTACTCTTGTGCCAGGGTGTGGTCTCCGACTACAAGGACGACGACGACGTGGACGCGGCC  132

Qy   41  AlaLeuAlaAlaProPheAspAspAspAspLysIleValGlyGlyTyr---AlaLeuAsp  59
         ||||                                             |||
Db  133  GCTCTTGCTGCCCCCTTTGATGATGACAAGATCGTTGGGGGCTACAACTGTTCTAGAG  192

Qy   60  ValAspSerTrpProTrpGlnValSerIleGlnTyrAspLysGlnHisValCysGlyGly  79
         |||                            :::
Db  193  CCCGGCACTCGCAGCCCTGGCAGCGGCGGCACTGGTCATGAAAACGAATTGTTCTGCTCGGGC  252

Qy   80  SerIleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAsp  99
         ||||:::||                          :::
Db  253  GTCCTGGTGCATCCGCAGTGGGTGCTGCTCAGCGCACACTGTTTCCAGAAC---------  303

Qy  100  ValPheAsnTrpLysValArgAlaGlyAlaAlaGlySerAspLysSerLeu-----GlySerPheProSer  117
         :::                                                  |||
Db  304  ------TCCTACACCATCGGGCTGGCCTGCAGTCTTGAGGCCTGACCAAGAGCCAGGG  357

Qy  118  LeuAlaValAlaLysIleIleIleIleGluPheAsnProMetTyrProLysAsp-----  135
         ||||                                                      
Db  358  AGCCAGATGGTGAGGGCCAGCCTCTCCGGTACGGGACCACCCAGAGTACAACAGACCCTTGCTC  417

Qy  136  --AsnAspIleAlaLeuMetLysLeuGlnPhePheProLeuThrPheSerGlyThrValArg  154
           :::                                                    ||||:::
Db  418  GCTAACGGTCTCATCGAAGTTGGACAAGTCCGTGTCCAGCTGACCACCATCCGG  477

Qy  155  ProIleCysLeuProPheAspGluLeuThrProAlaThrProLeuTrpIleIle  174
         |||                                                ::::
Db  478  AGCATCAGCATTGCT------TCGCAGTGCCTACCGCGGGGACTCTTGCTCGTTTCT  531

Qy  175  GlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeuLeuGlnAlaSer  194
         ||||||                                          :::||
Db  532  
```

```
Db   532 GGCTGGGTCTGCTGGCG------AACGGCGAGAATGCCTACCCTGCTGCAGTGCCTGAAC 585
                                ||||                    |||      ||||:|||||    ||||||||
Qy   195 ValGlnValIleAspThrArgCysAsnAla------AspAspAlaTyrArgGlnGlyGlu 212
Db   586 GTGTCGGTGGTGTCTGCAGTAAGCTGCTCATGACCCGCTGTACCAC------ 639
                                       ||||:||    :::    |||
Qy   213 ValThrGluLysMetMetCysAlaGlyLeuProGluGlyGlyGlyValAspThrCysGlnGly 232
Db   640 ------CCCAGCATGTTCTGCGCCGCGGGAGGCACGACCAGAAGGACTCCTGCAACGGT 693
                                              ||:|    |:|    ||||||
Qy   233 AspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIleIleValSer 252
Db   694 GACTCTGGGGGGGCCCCTGATCTGCAACGGG------TACTTGCAGGGCCTTGTGTCT 744
                                :::::||||||||    |:|:    |||||||||
Qy   253 TrpGlyTyrGly--CysGlyGlyProSerThrProGlyValThrTyrThrLysValSerAla 271
Db   745 TTCGGAAAAGCCCCGTGTGCCAAGTGGCTGTCTACACCAACCTCTGCAAA 804
                                :::|||    |||||||    |:    :::
Qy   272 TyrLeuAsnTrpIleTyrAsnValPheLysLeuSerArgHisHisHisHis 291
Db   805 TTCACTGAGTGGATAGAGAGAAAACCGTCCAGGCCAGT--TCTAGACATCACCATCACCAT 861
                                :::|||        :::
Qy   292 His 292
          |||
Db   862 CAC 864
```

```
RESULT 12
US-09-370-838-80
; Sequence 80, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
;       APPLICANT: Reed, Steven G.
;       APPLICANT: Lodes, Michael J.
;       APPLICANT: Mohamath, Roadoh
;       APPLICANT: Secrist, Heather
;       TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;       TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;       FILE REFERENCE: 210121.475C1
;       CURRENT APPLICATION NUMBER: US/09/370,838
;       CURRENT FILING DATE: 1999-08-09
;       EARLIER APPLICATION NUMBER: US 09/285,323
;       EARLIER FILING DATE: 1999-04-02
;       NUMBER OF SEQ ID NOS: 289
;       SOFTWARE: FastSEQ for Windows Version 3.0
;       SEQ ID NO 80
;       LENGTH: 1460
;       TYPE: DNA
;       ORGANISM: Homo sapien
US-09-370-838-80
```

```
Alignment Scores:
Pred. No.:                      1.31e-48          Length:          1460
Score:                          526.50            Matches:         97
Percent Similarity:             62.93%            Conservative:    49
Best Local Similarity:          41.81%            Mismatches:      79
Query Match:                    32.91%            Indels:          7
DB:                             4                 Gaps:            4

US-09-607-745-9 (1-292) x US-09-370-838-80 (1-1460)

Qy    49 AspAspLysIleValGlyLyrAlaLeuAspValAspSerTrpProTrpGlnValSer 68
                                :::    ||||||||||||            ::
Db   601 GAGCAGAGAATCCTTGGAGCACTGGAGGCTGGATGTGAGCAGGGAAGCTGGCCGTGGCAAGTCAGT 660
Qy    69 IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuLeuAspProHisTrpValLeu 88
                                :::    |||    ||||||:    :::||||
Db   661 CTGCGGCTCAATAATGCCCCACCACTGTGGAGGCAGCCTGATCAATAAACATGTGGATCCTG 720
Qy    89 ThrAlaAlaHisCysPheArgLysHisAspValPheAsnTrpLysValArgAlaGly 108
                                :::    ||||||:::||
Db   721 ACAGCAGCTCACTGCTTCAGAAGCAACTCTAATCCTCGTGACTGGTTGCCACGTCTGGT 780
Qy   109 SerAspLysLeuGlySerPheProSerLeu------AlaAlaLaLysIleIleIleIle 126
```

```
Db   781 ATTTCCACA------ACATTTCCTAAACTAAGAACTAAGAATGAGAGTAAGAAATATTTAATTCAT 834
                                :::||||||    ||||||    :::|||    |||
Qy   127 GluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPhePro 146
Db   835 AACAATTATAAATCTGCAACTCATGAAAATGACATTGCACTTGTGAGACTTGAGAACAGT 894
                                :::|||||:    :::|||    :::
Qy   147 LeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThr 166
Db   895 GTCACCTTACCAAAGATATCCATAGTGTGTTCTTCCCAGTCGTACCCAGAATATTCCA 954
                                ::|||||    :::|||
Qy   167 ProAlaThrProLeuTrpIleIleGlyTrpHisGlyPheThrLysGlnAsnGlyGlyLysMet 186
Db   955 CCTGGCTCTACTGCTTATGTAACAGGATGGGGCGGCTCAAGAATATGCTGGCCACACAGTT 1014
                                :::|||||    ::|||    :::
Qy   187 SerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAsp 206
Db  1015 CCAGAG--CTAAGGCAAGGACAGTCAGAATAATAAGTAATGATGTATGTAATGCACCA 1071
                                :::
Qy   207 AspAlaTyrGlnGlyGluValThrGlyGluLysMetCysAlaGlyIleIleProGluGlyIleGly 226
Db  1072 CATAGTTATAATGGAGCCATCTTGTCTGGAATGCTGTGTGCTGGAGTACCTCAAGGTGGA 1131
                                :::    ||    :::
Qy   227 ValAspThrCysGlnGlyLysAspSerGlyGlyProLeuMetTyrGlnSerAspGln------ 244
Db  1132 GTGGACGCATGTCAGGGTGACTCTGGTGGCCCACTAGTACAAGAAGACTCACGGCGGCT 1191
                                :::    :::
Qy   245 TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGly 264
Db  1192 TGGTTTATTGTGGGATAGTAAGCTGGGAGATCAGTGGGGAGGATCAGTGTGGCCTGCCGATAAGCCAGGA 1251
                                :::||||    ::|||
Qy   265 ValTyrThrLysValSerAlaTyrLeuAsnTrpIle 276
Db  1252 GTGTATCTGGAGTGACAGCCTACCTTGACTGGATT 1287
```

```
RESULT 13
US-08-508-448C-15
; Sequence 15, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
;       APPLICANT: Kazuyoshi YAMAOKA et al.
;       TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
;       TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Wenderoth, Lind & Ponack
;          STREET: 805 Fifteenth Street, N.W., #700
;          CITY: Washington
;          STATE: D.C.
;          COUNTRY: U.S.A.
;          ZIP: 20005
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: MS-DOS
;          SOFTWARE: Wordperfect 5.1
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/508,448C
;          FILING DATE: July 28, 1995
;          CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER:
;          FILING DATE:
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Warren M. Cheek, Jr.
;          REGISTRATION NUMBER: 33,367
;          REFERENCE/DOCKET NUMBER:
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 202-371-8850
;          TELEFAX:
;          TELEX:
; INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
```

```
;     APPLICANT: Reed, Steven G.
;     APPLICANT: Lodes, Michael J.
;     APPLICANT: Mohamath, Roadoh
;     APPLICANT: Secrist, Heather
;     TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;     TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;     FILE REFERENCE: 210121.475C1
;     CURRENT APPLICATION NUMBER: US/09/370,838
;     CURRENT FILING DATE: 1999-08-09
;     EARLIER APPLICATION NUMBER: US 09/285,323
;     EARLIER FILING DATE: 1999-04-02
;     NUMBER OF SEQ ID NOS: 289
;     SOFTWARE: FastSEQ for Windows Version 3.0
;     SEQ ID NO 79
;        LENGTH: 2790
;        TYPE: DNA
;        ORGANISM: Homo sapien
US-09-370-838-79

Alignment Scores:
Pred. No.:                              Length:        2790
Score:                 3.27e-48         Matches:         97
Percent Similarity:    62.93%           Conservative:    49
Best Local Similarity: 41.81%           Mismatches:      79
Query Match:           32.91%           Indels:           7
DB:                                     Gaps:             4

US-09-607-745-9 (1-292) x US-09-370-838-79 (1-2790)

Qy    49 AspAspLysIleValGlyGlyTyrAlaAlaLeuAspValAspSerTrpProTrpGlnValSer    68
Db   597 GAGCAGAGAATCCTTGGAGCGCACTGAGGCTGAGGAGGAAGCTGGCCGTGGCAAGTCAGT    656

Qy    69 IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu    88
Db   657 CTGCGGCTCAATAATGCCCACCACTGTGGAGGCAGCCTGATCAATAACATGTGGATCCTG    716

Qy    89 ThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGly   108
Db   717 ACAGCAGCTCACTGCTTCAGAAGCAACTCTAATCCTCGTGACTGGATTGCCACGTCTGGT    776

Qy   109 SerAspLysLeuGlySerPheProSerLeu-----AlaValAlaLysIleIleIleIle   126
Db   777 ATTTCCACA------ACATTTCCTAAACTAAGAATAGAGAATAAGAAAAATATTTTAATTCAT    830

Qy   127 GluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPhePro   146
Db   831 AACAATTATAAAATCGCAACTCATGAAAAATGACATTGCACTTGTGAGAACAGT    890

Qy   147 LeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThr   166
Db   891 GTCACCTTTACCAAAGATATCCATAGTGTGTCTCCCAGCTGCTACCCAGAATATTCCA    950

Qy   167 ProAlaThrProLeuTrpIleIleGlyTrpPheThrLysGlnAsnGlyGlyLysMet   186
Db   951 CCTGGCTCCTACTGCTTATGTAACAGGATGGGCGCTCAAGATAATGTGGCCACACAGTT   1010

Qy   187 SerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAsp   206
Db  1011 CCAGAG---CTAAGGACAAGGACAGTCAGAATAATAAGTAAGTATGTAATGCACCA   1067

Qy   207 AspAlaTyrGlnGlyGlyValThrGluLysMetMetCysAlaGlyIleIleProGluGluGlyGly   226
Db  1068 CATAGTTATAATGAGGCCATCTTGTCTGGAGTACCTCAAGGTGGA   1127

Qy   227 ValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGln------   244
Db  1128 GTGGACCGCATGTCAGGTGACTCTGGTGGCCCCACTAGTACAAGAAGACTCACGGCGGCTT   1187

Qy   245 TrpHisValGlyIleValSerTrpGlyTyrGlyCysGlyProSerThrProGly   264
Db  1188 TGGTTTATTGTGGGGATAGTAAGCTGTGGGGGAGGATCAGTGTGGCCTGCCGGATAAGCCAGGA   1247
```

```
;     LENGTH: 1517 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA to mRNA
;     ORIGINAL SOURCE:
;        ORGANISM: Homo sapiens
;        TISSUE TYPE: trachea
US-08-508-448C-15

Alignment Scores:
Pred. No.:                              Length:        1517
Score:                 1.38e-48         Matches:         97
Percent Similarity:    62.93%           Conservative:    49
Best Local Similarity: 41.81%           Mismatches:      79
Query Match:           32.91%           Indels:           7
DB:                                     Gaps:             4

US-09-607-745-9 (1-292) x US-08-508-448C-15 (1-1517)

Qy    49 AspAspLysIleValGlyGlyTyrAlaAlaLeuAspValAspSerTrpProTrpGlnValSer    68
Db   611 GAGCAGAGAATCCTTGGAGCGCACTGAGGCTGAGGAGGAAGCTGGCCGTGGCAAGTCTGGT    670

Qy    69 IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu    88
Db   671 CTGCGGCTCAATAATGCCCACCACTGTGGAGGCAGCCTGATCAATAACATGTGGATCCTG    730

Qy    89 ThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGly   108
Db   731 ACAGCAGCTCACTGCTTCAGAAGCAACTCTAATCCTCGTGACTGGATTGCCACGTCTGGT    790

Qy   109 SerAspLysLeuGlySerPheProSerLeu-----AlaValAlaLysIleIleIleIle   126
Db   791 ATTTCCACA------ACATTTCCTAAACTAAGAAGTAGAGAATTTTAATTCAT    844

Qy   127 GluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPhePro   146
Db   845 AACAATTATAAAATCGCAACTCATGAAAAATGACATTGCACTTGTGAGAACAGT    904

Qy   147 LeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThr   166
Db   905 GTCACCTTTACCAAAGATATCCATAGTGTGTCTCCCAGCTGCTACCCAGAATATTCCA    964

Qy   167 ProAlaThrProLeuTrpIleIleGlyTrpPheThrLysGlnAsnGlyGlyLysMet   186
Db   965 CCTGGCTCCTACTGCTTATGTAACAGGATGGGCGCTCAAGATAATGTGGCCACACAGTT   1024

Qy   187 SerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAsp   206
Db  1025 CCAGAG---CTAAGGACAAGGACAGTCAGAATAATAAGTAAGTATGTAATGCACCA   1081

Qy   207 AspAlaTyrGlnGlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGly   226
Db  1082 CATAGTTATAATGAGGCCATCTTGTCTGGAGTACCTCAAGGTGGA   1141

Qy   227 ValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGln------   244
Db  1142 GTGGACCGCATGTCAGGTGACTCTGGTGGCCCCACTAGTACAAGAAGACTCACGGCGGCTT   1201

Qy   245 TrpHisValGlyIleValSerTrpGlyTyrGlyCysGlyProSerThrProGly   264
Db  1202 TGGTTTATTGTGGGGATAGTAAGCTGTGGGGGAGGATCAGTGTGGCCTGCCGGATAAGCCAGGA   1261

Qy   265 ValTyrThrLysValSerAlaTyrLeuAsnTrpIle   276
Db  1262 GTGTATACTCGAGTGACAGCCTACCTTGACTGGATT   1297

RESULT 14
US-09-370-838-79
;  Sequence 79, Application US/09370838
;  Patent No. 644425
;  GENERAL INFORMATION:
```

```
Qy    265  ValTyrThrLysValSerAlaTyrLeuAsnTrpIle  276
           |||||||||||:||:|||:|||:|||:|||
Db   1248  GTGTATACTCGAGTGACAGCCTACCTTGACTGGATT  1283
```

RESULT 15
US-09-370-838-55
; Sequence 55, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
;   LENGTH: 1462
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-370-838-55

Alignment Scores:
Pred. No.:   Length: 1462
Score: 524.50   Matches: 96
Percent Similarity: 62.93%   Conservative: 50
Best Local Similarity: 41.38%   Mismatches: 79
Query Match: 32.78%   Indels: 7
DB: Gaps: 4

US-09-607-745-9 (1-292) x US-09-370-838-55 (1-1462)

```
Qy     49  AspAspLysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSer   68
           ::   :::: |||:::                   ::
Db    597  GAGCAGAGAATCCTTGGAGGCACTGAGGCTGAGGAGGGAAGCTGGCCGTGGCAACTCAGT  656

Qy     69  IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu   88
           : ::::  |||:|||||||::::||||||||||||||||||||::::||||::|||||
Db    657  CTGCGGCTCAATAATGCCCACCACTGTGGAGGCAGCCTGATCAATAACATGTGGATCCTG  716

Qy     89  ThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGly  108
           ||||||||||::   :::::::::       |||||  :: |||
Db    717  ACAGCAGCTCACTGCTTCAGAAGCAACTCTAATCCTCGTGACTGGATTGCCACGTCTGGT  776

Qy    109  SerAspLysGlySerPheProSerLeu------AlaValAlaLysIleIleIleIleIle  126
           :::||   :::-----ACATTCCTAAACTAAGAGAATGAGATAAGAAATATTTAATTCAT  830
Db    777  ATTTCCACA------ACATTCCTAAACTAAGAGAATGAGATAAGAAATATTTAATTCAT  830

Qy    127  GluPheAsnProMetTyrProLysAspAsnIleAlaLeuMetLysLeuGlnPhePro  146
           |||       :: :::
Db    831  AACAATTATAAATCTGCAACTCATGAAAATGACATTGCACTTGTGAGACTTGAGAACAGT  890

Qy    147  LeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThr  166
           :::||||||||    ||||                  :::
Db    891  GTCACCTTTACCAAAGATATCCATAGTGTGTCTCCCAGCTGCTACCCAGAATATTCCA  950

Qy    167  ProAlaThrProLeuTrpIleLeuGlyTrpProGlyPheThrLysGlnAsnGlyGlyLysMet  186
           |||    :::    :: |||||           ||   |||   :::
Db    951  CCTGGCTCTACTGCTTATGTAACAGGATGGGGCGGCCTCAAGAATATGCTGCCACACAGTT  1010

Qy    187  SerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAsp  206
           :::  |||    ::: |||           :::
Db   1011  CCAGAG---CTAAGGCAAGGACAGGTCAGAATAAATAAGTAAGTAATGATGTAATGCACCA  1067

Qy    207  AspAlaTyrGlnGlyGluValThrGluLysMetCysAlaGlyIleProGluGlyGlyGly  226
           |:||:|||||      ||| |||::|||:|||||||||||:|||:|||:||
Db   1068  CATAGTTATAATGGAGCCATCTTGTCTGGAATTGCTGTGTGCTGGAGTACCTCAAGGTGGA  1127
```

```
Qy    227  ValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGln------  244
           |||||   ||||||||||||||||||||||||||||:|||||:|||||:||:
Db   1128  GTGGACGACGATGTCAGGGTGACCTGGTGGCCCAGTACAAGAAGACTCACGGCGGCTT  1187
```

```
Qy    245  TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGly  264
           :::      ::|||||||||||||||:|||||||||||||||||||| |||
Db   1188  TGGTTTATTGTGGGGATAGTAAGCTGGGGGGAGATCAGTGTGGCCTGCCGGATAAGCCAGGA  1247
```

```
Qy    265  ValTyrThrLysValSerAlaTyrLeuAsnTrpIle  276
           |||||||||||:||:|||:|||:|||:|||
Db   1248  GTGTATACTCGAGTGACAGCAGCCATACATTGACTGGATT  1283
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Search completed: December   2, 2003, 02:54:22
Job time : 64.2311 secs

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    December  2, 2003, 02:42:05 ; Search time 391.32 Seconds
                                         (without alignments)
                                         3662.446 Million cell updates/sec

Title:     US-09-607-745-2
Perfect score: 2342
Sequence:  1 MDPDSDQPLNSLDVKPLRKP.......VTTKVSAVLNWIYNVWKAEL 435

Scoring table: BLOSUM62
           Xgapop  10.0 , Xgapext   0.5
           Ygapop  10.0 , Ygapext   0.5
           Fgapop   6.0 , Fgapext   7.0
           Delop    6.0 , Delext    7.0

Searched:     2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters:     4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool_p/US09607745/runat_01122003_160940_10006/app_query.fasta_1.1038
 -DB=Published_Applications_NA: -QFMT=fasta -SUFFIX=rnpb -MINMATCH=0.1
 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
 -MAXLEN=200000000 -USER=US09607745 @CGN_1_129 @runat_01122003_160940_10006
 -NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
             1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
             2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
             3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
             4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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             6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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            14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
            15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
            16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
            17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

                              SUMMARIES
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2338	99.8	2038	12	US-10-180-719-18	Sequence 18, Appl

2	2337	99.8	2081	9	US-09-851-588-7	Sequence 7, Appli
3	2337	99.8	2307	14	US-10-097-340-317	Sequence 317, App
4	2337	99.8	2307	14	US-10-171-311-217	Sequence 217, App
5	2329	99.4	2165	12	US-10-101-510-634	Sequence 634, App
6	2324	99.2	2079	9	US-09-851-588-5	Sequence 5, Appli
7	2324	99.2	2079	11	US-09-776-191-71	Sequence 71, Appl
8	2324	99.2	2079	14	US-10-264-820-22	Sequence 22, Appl
9	2324	99.2	2079	14	US-10-254-289-1	Sequence 1, Appli
10	2319	99.0	2137	11	US-09-776-191-3	Sequence 3, Appli
11	2297.5	98.1	2063	11	US-09-888-257A-2	Sequence 2, Appli
12	2297.5	98.1	2063	11	US-09-946-374-274	Sequence 274, App
13	2297.5	98.1	2063	12	US-10-015-387A-274	Sequence 274, App
14	2297.5	98.1	2063	12	US-10-063-735-111	Sequence 111, App
15	2297.5	98.1	2063	12	US-10-006-130A-274	Sequence 274, App
16	2297.5	98.1	2063	12	US-10-199-672-329	Sequence 329, App
17	2297.5	98.1	2063	12	US-10-006-172A-274	Sequence 274, App
18	2297.5	98.1	2063	12	US-10-187-749-329	Sequence 329, App
19	2297.5	98.1	2063	12	US-10-194-457-329	Sequence 329, App
20	2297.5	98.1	2063	12	US-10-184-642-329	Sequence 329, App
21	2297.5	98.1	2063	12	US-10-196-747-329	Sequence 329, App
22	2297.5	98.1	2063	12	US-10-015-392A-274	Sequence 274, App
23	2297.5	98.1	2063	12	US-10-017-253A-274	Sequence 274, App
24	2297.5	98.1	2063	12	US-10-173-689-329	Sequence 329, App
25	2297.5	98.1	2063	12	US-10-173-690-329	Sequence 329, App
26	2297.5	98.1	2063	12	US-10-173-691-329	Sequence 329, App
27	2297.5	98.1	2063	12	US-10-173-692-329	Sequence 329, App
28	2297.5	98.1	2063	12	US-10-173-694-329	Sequence 329, App
29	2297.5	98.1	2063	12	US-10-173-698-329	Sequence 329, App
30	2297.5	98.1	2063	12	US-10-173-699-329	Sequence 329, App
31	2297.5	98.1	2063	12	US-10-173-707-329	Sequence 329, App
32	2297.5	98.1	2063	12	US-10-174-569-329	Sequence 329, App
33	2297.5	98.1	2063	12	US-10-174-583-329	Sequence 329, App
34	2297.5	98.1	2063	12	US-10-174-587-329	Sequence 329, App
35	2297.5	98.1	2063	12	US-10-174-589-329	Sequence 329, App
36	2297.5	98.1	2063	12	US-10-174-591-329	Sequence 329, App
37	2297.5	98.1	2063	12	US-10-175-736-329	Sequence 329, App
38	2297.5	98.1	2063	12	US-10-175-742-329	Sequence 329, App
39	2297.5	98.1	2063	12	US-10-175-744-329	Sequence 329, App
40	2297.5	98.1	2063	12	US-10-175-745-329	Sequence 329, App
41	2297.5	98.1	2063	12	US-10-175-748-329	Sequence 329, App
42	2297.5	98.1	2063	12	US-10-175-751-329	Sequence 329, App
43	2297.5	98.1	2063	12	US-10-175-754-329	Sequence 329, App
44	2297.5	98.1	2063	12	US-10-176-480-329	Sequence 329, App
45	2297.5	98.1	2063	12	US-10-176-489-329	Sequence 329, App

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                              ALIGNMENTS

RESULT 1
US-10-180-719-18
; Sequence 18, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;              Hillman, Jennifer L.
;              Yue, Henry
;              Guegler, Karl J.
;              Corley, Neil C.
;              Tang, Tom Y.
;              Shah, Purvi
;   TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
;   NUMBER OF SEQUENCES: 24
;   CORRSPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Dr.
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
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; SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/180,719
    FILING DATE: 25-Jun-2002
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/008,271
    FILING DATE: 16-Jan-1998
ATTORNEY/AGENT INFORMATION:
    NAME: Mohan-Peterson, Sheela
    REGISTRATION NUMBER: 41,201
    REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-855-0555
    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2038 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    IMMEDIATE SOURCE:
        LIBRARY: COLNNOT13
        CLONE: 1337018
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-180-719-18

Alignment Scores:
Pred. No.:              6.8e-283          Length:        2038
Score:                  2338.00           Matches:       434
Percent Similarity:     100.00%           Conservative:  1
Best Local Similarity:  99.77%            Mismatches:    0
Query Match:            99.83%            Indels:        0
DB:                     12                Gaps:          0

US-09-607-745-2 (1-435) x US-10-180-719-18 (1-2038)

Qy    1 MetAspProAspSerAspGlnProLeuAsnSerLeuAspValValLysProLeuArgLysPro   20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  200 ATGGATCCTGACAGTGATCAACCTCTGAACAGCCTGATGTCAAACCCTGCGCAAACCC        259

Qy   21 ArgIleProMetGluThrPheArgLysValGlyIleProIleIleAlaLeuLeuSer          40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  260 CGTATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCATCATCATAGCACTACTGAGC        319

Qy   41 LeuAlaSerIleIleIleValValLeuLeuLysValIleLeuAspValTyrTyrPhe          60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  320 CTGGCGAGTATCATCATTGTGGTTCTCCTCATCAAGGTGATTCTGGATAAATACTACTTC      379

Qy   61 LeuCysGlyGlnProLeuHisProIlePheIleProArgLysGlnLeuCysAspGlyGluLeuAsp  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  380 CTCTGCGCGGAACCCTCCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGAC      439

Qy   81 CysProLeuGlyLeuGluAspGluHisCysValLysSerValLysSerPheProGluProAlaVal 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  440 TGTCCCTTGGGGACGAGCAGAGCAGGAGACGCTTCCCCGAAGGGCCTGCAGTG            499

Qy  101 AlaValArgLeuSerLysAspAspArgSerThrLeuGlnValLeuAspAspSerAlaThrGlyAsn 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  500 GCAGTCCGCCTCTCCAAGGACGACCGATCACCACTCCAGGTGCTGGACTGCCGGCCACAGGGAAC 559

Qy  121 TrpPheSerAlaCysPheAspAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln    140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  560 TGGTTCTCTGCCTGTTTCGACACTTCACAGAAGCTCTGCTGAGACAGCGCTGTAGGCAG       619

Qy  141 MetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyLysProAspGlnAspLeu   160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  620 ATGGGCTACAGCAGCAAACCCACCTTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTG     679

Qy  161 AspValValGluIleThrGluAsnSerGlnAsnSerGlnLeuLeuArgMetArgAsnSerSerGlyPro 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  680 GATGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGAACTCAAGTGGGCCC       739

Qy  181 CysLeuSerGlySerLeuValSerLeuHisCysLeuLeuAlaCysGlyLysGlyLysSerLeuLysThr 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  740 TGTCTCTCAGGTCCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGGAGGAGCCTGAAGACC     799

Qy  201 ProArgValValGlyGluUAlaSerValAlaSerProTrpProGlnValSerIle           220
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  800 CCCCGGTGGTGGGTGGGGAGGAGCCTCTGGGATTCTTGCCTTGCCAGGTCAGCATC          859

Qy  221 GlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThr       240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  860 CAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCCTCACG       919

Qy  241 AlaAlaHisCysPheArgLysHisThrAspValPheAsnThrLysValArgAlaGlySer       260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  920 GCAGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGTGCGGGCAGGCTCA       979

Qy  261 AspLysGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleIleGluPheAsn       280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  980 GACAAACTGGGCAGCTTCCCATCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAAC      1039

Qy  281 ProMetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheAlaProLeuThrPhe      300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1040 CCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTC     1099

Qy  301 SerGlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThr        320
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1100 TCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACC    1159

Qy  321 ProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIle      340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1160 CCACTCTGGATCATTGATGGGTTTACAAGCAGAATGAGGGGAAGATGTCTGACATA        1219

Qy  341 LeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyr      360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1220 CTGCTGCAGGGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTAC     1279

Qy  361 GlnGlyGluValThrGluLysMetCysAlaGlyTyrIleProGluGlyGlyValAspThr     380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1280 CAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGACACC     1339

Qy  381 CysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspLysTrpHisValValGly     400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1340 TGCCAGGGTGACAGTGGTGGCCCCCTGATGTACCAATCTGACAAGTGGCATGTGGTGGGC    1399

Qy  401 IleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVal     420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1400 ATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACCACCAAGGTC   1459

Qy  421 SerAlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu                 435
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 1460 TCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG                    1504
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;     ORGANISM: Homo sapiens
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (215)..(1528)
;     OTHER INFORMATION:
US-09-851-588-7

Alignment Scores:
Pred. No.:             9.38e-283        Length:          2081
Score:                 2337.00          Matches:         434
Percent Similarity:    100.00%          Conservative:    0
Best Local Similarity: 100.00%          Mismatches:      0
Query Match:           99.79%           Indels:          0
DB:                    9                Gaps:            0

US-09-607-745-2 (1-435) x US-09-851-588-7 (1-2081)
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Qy      2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg    21
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    224 GATCCTGACAGTGATCATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCGT   283

Qy     22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu    41
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCATCATCATAGCACTACTGAGCCTG    343

Qy     42 AlaSerIleIleIleValValLeuIleLeuIleValIleLeuLysValAspLysTyrTyrPheLeu    61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 GCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTCTGGATAAAATACTACTTCCTC   403

Qy     62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys    81
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 TGCGGGCAGCCTCTCCACTTCATCCCGAGAAAGCAGCTGTGTGACGGAGAGCTGGACTGT   463

Qy     82 ProLeuGlyGluAspGluHisCysValLysSerValLysSerPheProGluGlyProAlaValAla   101
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 CCCTTGGGGGAGGACGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA   523

Qy    102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp   121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 GTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAACTGG   583

Qy    122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaLeuThrAlaCysArgGlnMet   141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 TTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGCACAGCGTGTAGGCAGATG   643

Qy    142 GlyTyrSerSerIysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp   161
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 GGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGAT   703

Qy    162 ValValGluIleThrGluAsnSerGlnLeuLeuArgMetArgAsnSerSerGlyProCys   181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 GTTGTTGAAATCACAGAAAATCACAGGAGAGCTTCGACATGCGAACTCAAGTGGGCCCTGT   763

Qy    182 LeuSerGlySerLeuValSerLeuValHisCysSerLeuAlaCysSerGlyLeuLysThrPro   201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    764 CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAGAGCCTGAAGACCCCC   823

Qy    202 ArgValValGlyGlyGluLeuAlaSerValAspSerTrpProTrpGlnValSerIleGln   221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 CGTGTGGTGGGTGGGGAGGCCCTCTGTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG   883

Qy    222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla   241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA   943

Qy    242 AlaHisCysPheArgLysHisThrAspValPheAsnValTrpLysValAlaArgAlaGlySerAsp   261
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGGCGCGGGCAGGCTCAGAC  1003

Qy    262 LysLeuGlyLysSerPheProSerLeuAlaValAlaAlaLysIleIleIleGluPheAsnPro   281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 AAACTGGGCAAGTCTTCCATCCTCGGCTGTGGCCAAGATCATCATTGAATTCAACCCC  1063
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Qy    282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer   301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 ATGTACCCCAAAGACAATGACATGACGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA  1123

Qy    302 GlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPro   321
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 GGCACAGTCAGGCCCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCCA  1183

Qy    322 LeuTrpIleIleGlyTrpGlyPheThrLysGluGlnAsnGlyLysMetSerAspIleLeu   341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGGAAGATGTCTGACATACTG  1243

Qy    342 LeuGlnAlaSerValGlnValIleAlaSerProThrArgCysAsnAlaAspAlaTyrGln   361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1244 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACGTCAATGCAGCACGATGCGTACCAG  1303

Qy    362 GlyGluValThrGluLysLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys   381
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1304 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAGGGGGTGGACACTTGC  1363

Qy    382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle   401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1364 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC  1423

Qy    402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer   421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1424 GTTAGCTGGGGCTATGGCTGCGGGGGCCCAGCACCCCCAGGAGTATACACCAAGGTCTCA  1483

Qy    422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu   435
            |||||||||||||||||||||||||||||||||||||
Db   1484 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG  1525
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RESULT 3
US-10-097-340-317
; Sequence 317, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
   APPLICANT: John MONAHAN
   APPLICANT: Manjula GANNAVARAPU
   APPLICANT: Sebastian HOERSCH
   APPLICANT: Shubhangi KAMATKAR
   APPLICANT: Steve G. KOVATS
   APPLICANT: Rachel E. MEYERS
   APPLICANT: Michael MORRISEY
   APPLICANT: Peter OLANDT
   APPLICANT: Ami SEN
   APPLICANT: Peter VEIBY
   APPLICANT: Gordon B. MILLS
   APPLICANT: Robert C. BAST, Jr.
   APPLICANT: Karen LU
   APPLICANT: Rosemarie SCHMANDT
   APPLICANT: Xumei ZHAO
   APPLICANT: Karen GLATT
   TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
   TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
   FILE REFERENCE: MRI-030
   CURRENT APPLICATION NUMBER: US/10/097,340
   CURRENT FILING DATE:  2002-03-14
   PRIOR APPLICATION NUMBER: 60/276,025
   PRIOR FILING DATE: 2001-03-14
   PRIOR APPLICATION NUMBER: 60/325,149
   PRIOR FILING DATE: 2001-09-26
   PRIOR APPLICATION NUMBER: 60/276,026
   PRIOR FILING DATE: 2001-03-14
   PRIOR APPLICATION NUMBER: 60/324,967
   PRIOR FILING DATE: 2001/09/26
   PRIOR APPLICATION NUMBER: 60/311,732
   PRIOR FILING DATE: 2001-08-10
   PRIOR APPLICATION NUMBER: 60/325,102
   PRIOR FILING DATE: 2001-09-26
   PRIOR APPLICATION NUMBER: 60/323,580
   PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2307)
; OTHER INFORMATION: n = A,T,C or G
US-10-097-340-317

Alignment Scores:

Pred. No.:   1.1e-282   Length: 2307
Score: 2337.00   Matches: 434
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 99.79%   Indels: 0
DB: Gaps: 0

US-09-607-745-2 (1-435) x US-10-097-340-317 (1-2307)

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Qy     2  AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg   21
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   284  GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCTGGGCAAACCCCGT  343

Qy    22  IleProMetGluThrPheArgLysValGlyIleProIleIleIleIleAlaLeuLeuSerLeu   41
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   344  ATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATCATAGCACTACTGAGCCTG  403

Qy    42  AlaSerIleIleIleLeuValValLeuIleLysValIleLeuLeuAspLysTyrTyrPheLeu   61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   404  GCGAGTATCATCATCTTGTGGTTGTCCTCATCAAGGTGATAAATACTACTTCCTC  463

Qy    62  CysGlyGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyLeuAspCys   81
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464  TGCGGGGGACAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGAGAGCTGGACTGT  523

Qy    82  ProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAla   101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524  CCCTTGGGGGAGGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA  583

Qy   102  ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp   121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584  GTCCGCCTCTCCAAGACCGATCCACACTCCACTGCTGGACTCGGCCACAGGGAACTGG  643

Qy   122  PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaLeuGluThrAlaCysArgGlnMet   141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   644  TTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATG  703

Qy   142  GlyTyrSerSerLysProThrThrArgAlaValAlaValGluIleGlyProAspGlnLeuAsp   161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704  GGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAGATTGGCCCAGGACCTGGAT  763

Qy   162  ValValGluThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCys   181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   764  GTTGTTGAAATCACAGAAAAACGCCAGAGCTTCGACATGCGGACTCAAGTGGGCCCTGT  823

Qy   182  LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysSerThrPro   201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   824  CTCTCAGGGTCCCTGGTCTCCCTGCACTGTTTGGCTTGTGGGAAGAGCCTGAAGAGCACCCCA  883

Qy   202  ArgValValGlyGlyGluGluAlaSerValAlaSerValAspSerSerTrpProrpGlnVal   221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   884  CGTGTGGTGGGTGGGGAGGAGGCATCCTGAGGGAGCCCCACTGGGTCCTCAGCATCCAG  943

Qy   222  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla   241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   944  TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA  1003

Qy   242  AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp   261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1004  GCCCACTGCTTCAGGAAACATACGGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC  1063
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Qy   262  LysLeuGlySerPheProSerLeuAlaAlaValAlaLysIleIleIleIleGluPheAsnPro   281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1064  AAACTGGGCAGCTTCCCATCCCTGGCTGCCGTGGCCAAGATCATCATCATTGAATTCAACCCC  1123

Qy   282  MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnGlnProLeuThrPheSer   301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1124  ATGTACCCCAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA  1183

Qy   302  GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro   321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1184  GGCACAGTGAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA  1243

Qy   322  LeuTrpIleIleGlyTrpGlyPheThrLysValGlnAsnGlyGlyLysMetSerAspIleLeu   341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1244  CTCTGGATCATTGGATGGGGCTTTACGAAGGTACAGAACGGAGGGAAGATGTCTGACATACTG  1303

Qy   342  LeuGlnAlaSerValGlnValIleLeuAspArgSerThrArgCysAsnAlaAspProTyrGln   361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1304  CTGCAGGCGTCAGTCCAGGTCATTGACAGACACGGTCAATGCAGACGATGCGTACCAG  1363

Qy   362  GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValValAspThrCys   381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1364  GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC  1423

Qy   382  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspArgTrpHisValValGlyIleIle   401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1424  CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATTGACCAGTGGCATGGTGGGCATC  1483

Qy   402  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer   421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1484  GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA  1543

Qy   422  AlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeu   435
          |||||||||||||||||||||||||||||||||||||
Db  1544  GCCTATCTCAACTGGATCTACAATGTCTGAAGGCTGAGCTG  1585
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RESULT 4
US-10-171-311-217
; Sequence 217, Application US/10171311
; Publication No. US2003008270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720, 1724, 1728,
; LOCATION: 1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791, 1802, 1821,
; LOCATION: 1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012, 2038, 2143
; OTHER INFORMATION: n = A,T,C or G

US-10-171-311-217

Alignment Scores:
Pred. No.:
Score: 1.1e-282
                                2337.00   Length: 2307
Percent Similarity: 100.00%   Matches: 434
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 99.79%   Mismatches: 0
DB: Indels: 0
                                                 Gaps: 0

US-09-607-745-2 (1-435) x US-10-171-311-217 (1-2307)

```
Qy      2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGT 343

Qy     22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu 41
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATCATAGCACTACTGAGCCTG 403

Qy     42 AlaSerIleIleLeuValLeuValLeuLeuLysValIleLeuLysTyrTyrPheLeu 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 GCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATAAATACTACTTCCTC 463

Qy     62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 TGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGT 523

Qy     82 ProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAla 101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 CCCTTGGGGGAGGACGACGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA 583

Qy    102 ValArgLeuLysSerLysAspSerArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 GTCCGCCTCTCCAAGAAGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAACTGG 643

Qy    122 PheSerAlaCysPheAspAsnPheGluAlaLeuAlaGluThrAlaLeuAlaCysArgGlnMet 141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 TTCTCTGCCTGTTTCGACAACTTCGAAGCTCTCGCAGAGACTGCTCTGGCCTGTAGGCAGATG 703

Qy    142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 GGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGAT 763

Qy    162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCys 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    764 GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGCCCTGT 823

Qy    182 LeuSerGlySerLeuValSerLeuValSerLeuHisCysLeuAlaCysGlyLeuLysSerLeuLysSerLeuThrPro 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCC 883

Qy    202 ArgValValGlyValGlyGluAlaSerValAlaLysAlaAlaLysAlaLysAlaSerValSerProGlnValSerIleGln 221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 CGTGTGGTGGGGTGGGGGAGGAGGCCTCTGTGGCCAAGGCCCTTCGTGCGCAGTGTCAGCATCCAG 943

Qy    222 TyrAspLysGlnHisValCysGlyGlySerIleGluGlyAspProHisValTrpValLeuThrAla 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 TACGACAAAACAGCAGTCTGTGGAGGGAGCATCGAGGGAGGACCCCACTGGGTCCTCACGGCA 1003

Qy    242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGTCAGAC 1063

Qy    262 LysLeuGlySerPheProSerLeuAlaAlaLysAlaLysAlaIleLeuIleGluIleGluIleIleGluGluPheAsnPro 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 AAACTGGGCAGCTTCCCATCCCTGGCTGCCAAGATCATCATCATTGAATTCAACCCC 1123

Qy    282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrPheSer 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1183

Qy    302 GlyThrValArgProIleCysLeuProPheAspGluGluThrPro 321
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 GGCACAGTCAGGCCCATCTGCCTGCCCTTCGATGAGGAGCTCACTCCAGCCACCCCCA 1243

Qy    322 LeuTrpIleIleGlyTrpGlyPheThrLysLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1244 CTCTGGATCATTGGATGGGGCTTACGAGCAGAATGGAGGGAAGATGTCTGACATACTG 1303

Qy    342 LeuGlnAlaSerValGlnValAlaLeuAspSerThrArgCysAsnAlaAspAlaTyrGln 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1304 CTGCAGGCGTCAGTGCAGGTCGCACTGGACAGCACGCGTGCAATGCAGACGATGCGTACCAG 1363

Qy    362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1364 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACTTGC 1423

Qy    382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerGlnTrpHisValValGlyIle 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1424 CAGGGTGACAGTGGTGGTCCCCTGATGTACCAATCTGACCAGTGGCATGTGGGCATC 1483

Qy    402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1484 GTTAGCTGGGGCTATGGCTGCGGGGGCCCCAGCACCCCAGGAGTATACACCAAGGTCTCA 1543

Qy    422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysValAlaGluLeu 435
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1544 GCCTATCTCAACTGACTCACAATGTCTGGAAGGCTGAGCTG 1585
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RESULT 5
US-10-101-510-634
; Sequence 634, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 634
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-634

Alignment Scores:
Pred. No.:
Score: 1.01e-281
                                2329.00   Length: 2165
Percent Similarity: 99.77%   Matches: 435
Best Local Similarity: 99.77%   Conservative: 0
Query Match: 99.44%   Mismatches: 0
DB: Indels: 1
                                                 Gaps: 0

US-09-607-745-2 (1-435) x US-10-101-510-634 (1-2165)

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Qy      1 MetAspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysPro 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 ATGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCC 369

Qy     21 ArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 CGTATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGC 429

Qy     41 LeuAlaSerIleIleLeuValLeuValLeuLeuLysValIleLeuLysTyrTyrPhe 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATAAATACTACTTC 489

Qy     61 LeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAsp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 CTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGAC 549
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RESULT 6
US-09-851-588-5
; Sequence 5, Application US/09851588
; Patent No. US20020042067A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, A]
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-68829-1/DJB/JUD/AMS
; CURRENT APPLICATION NUMBER: US/09/851,588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 2079
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-588-5

Alignment Scores:
Pred. No.:   4.03e-281   Length: 2079
Score: 2324.00   Matches: 434
Percent Similarity: 99.77%   Conservative: 0
Best Local Similarity: 99.77%   Mismatches: 0
Query Match: 99.23%   Indels: 1
DB: Gaps: 0

US-09-607-745-2 (1-435) x US-09-851-588-5 (1-2079)

Qy   2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg   21
Db   217 GATCCTGACAGTGATCAACCTCTGAACAGCCTGGATGTCAAACCCTGCGCAAACCCCGT   276

Qy   22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuLeuSerLe   41
Db   277 ATCCCCATGGAGACGTTCAGAAAGTGTGGGGATCCCATCATCATAGACACTACTGAGCCT   336

Qy   41 uAlaSerIleIleIleValValLeuIleLysValIleLeuAspLysTyrTyrPheLe   61
Db   337 GGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATAATAATACTACTTCCT   396

Qy   61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuProArgGluGlyLeuAspCy   81
Db   397 CTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGACTG   456

Qy   81 sProLeuGlyAspGluHisCysValLysSerPheProGluGlyProAlaValAl   101
Db   457 TCCCTTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCCTGCAGTGGC   516

Qy   101 aValArgLeuSerLysAspArgSerAlaThrArgGlyAsnTr   121
Db   517 AGTCCGCCTCTCCAAGGACCGATCCACACTGCCAGTGCGTCGGCCACAGGGAACTG   576

Qy   121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrArgArgGlnMe   141
Db   577 GTTCTCTGCCTGTTCGACAACTTCACAGAAGCTCTGGCTGAGACCAGCCTGTAGGCAGAT   636

Qy   141 tGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspLeuAs   161
Db   637 GGGCTACAGCAGCAAACCCACCTTTCAGACGTGTGGAGATTGGCCCAGACCAGGATCTGGA   696

Qy   161 pValValGluThrGluAsnSerGlnLeuArgMetArgAsnSerGlyProCy   181
Db   697 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCCATGGGAACTCAAGTGGGCCCTG   756

Qy   181 sLeuSerGlySerLeuValSerLeuHisCysLeuLeuAlaCysGlyLysSerLeuThrPr   201
Db   1570 CTCCAGCCCTCATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG   1615

Qy   81 CysProLeuGlyAspGluHisCysValLysSerPheProGluGlyProAlaVal   100
Db   550 TGTCCCTTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCCTGCAGTG   609

Qy   101 AlaValArgLeuSerLysAspArgSerAlaThrArgGlyAsnTrpLeuAspSerAlaThrGlyAsn   120
Db   610 GCAGTCCGCCTCTCCAAGGACCGATCCACACTGCCAGTGCGTCGGCCACAGGGAAC   669

Qy   121 TrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluAlaGluThrArgArgAlaCysArgGln   140
Db   670 TGGTTCTCTGCCTGTTCGACAACTTCACAGAGCTCTGGCTGAGACCAGCAGCTGTGTAGGCAG   729

Qy   141 MetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnIleAspLeu   160
Db   730 ATGGGCTACAGCAGCAAACCCACCTTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTG   789

Qy   161 AspValValGluIleThrGluAsnSerGlnLeu-LeuArgMetArgAsnSerSerGlyPr   180
Db   790 GATGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCCATGGGAACTCAAGTGGGCC   849

Qy   180 oCysLeuSerGlySerLeuValSerLeuHisCysLeuLeuAlaCysGlyLysSerLeuLysSerTh   200
Db   850 CTGTCTCTCAGCCCTCATCTCAACTGGATCTACAATGTCTGGAAGAGCCTGAAGGAC   909

Qy   200 rProArgArgValValGlyGluGluValAlaSerValAspSerTrpProTrpGlnValSerIl   220
Db   910 CCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCAT   969

Qy   220 eGlnTyrAspLysGlnHisIleCysValCysGlyGlyValGlySerIleLeuAspProHisTrpPheValLeuTh   240
Db   970 CCAGTACGACAAAACAGCACAGTGTGTGTGGGGAGACCATCCTGGACCCCACTGGGTCCTCAC   1029

Qy   240 rAlaAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValIleArgAlaGlySe   260
Db   1030 GGCAGCCGCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTC   1089

Qy   260 rAspLysLysLeuGlySerPheProSerGluAlaAlaLysIleIleIleGluGluPheAs   280
Db   1090 AGACAAGCTGGGCAGCTTCCCATCCTGTGTGCCAAGATCATCATCATTGAATTCAA   1149

Qy   280 nProMetTyrProLysAspAspAsnAspIleAlaLeuMetLysLeuGluGlnProLeuThrPh   300
Db   1150 CCCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGCTGCCCACTCACTTT   1209

Qy   300 eSerGlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaTh   320
Db   1210 CTCAGGCACAGTGCAGCCCCATCGTGCTGCCCTTCTTTGACGAGGAGCTCACTCCCAGCCAC   1269

Qy   320 rProLeuTrpIleIleGlyTrpGlyPheThrArgGlnAsnGlyAsnGlyLyLyMetSerAspIl   340
Db   1270 CCCACTCTGGATCATTGGGGCTTTACGAAGCAGAATGGAGGAAGATGTCTGACAT   1329

Qy   340 eLeuLeuGlnAlaSerValGlnIleValIleAspSerThrArgCysAsnAlaAspAspAlaTy   360
Db   1330 ACTGCTGCAGGCGGTCAGTGCAGGTCCAGGAGCAATGCAGACGATGCGTA   1389

Qy   360 rGlnGlyGluValThrGluLysMetCysAlaGlyTyrIleProGlyGlyValAspGlyValGlyValAspTh   380
Db   1390 CCAGGGGGAGGTCACCGAGAAGATGATGTGCGCAGGCATCCCGAGAGGGGTGTGGACAC   1449

Qy   380 rCysSerGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGl   400
Db   1450 CTGCCAGGTGACAGTGGCCCCTGTGGGCCCCTGATGTACCAATCTGACCAGTGCATGTGTGGG   1509

Qy   400 yIleValSerTrpGlyTyrGlyCysGlyLysProSerThrProGlyValTyrThrLysVa   420
Db   1510 CATCGTTAGCTGGGGATACGGGTGCGGGGGGCCCAGCACCCCAGGAGTATACACCAAGGT   1569

Qy   420 lSerAlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysAlaGluLeu   435
Db   1570 CTCAGCCTACCTCAATCTACAATGTCTGGAAGGCTGAGCTG   1615

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Alignment Scores:
Pred. No.:                                              2079
Score:                 4.03e-281       Length:          2079
                        2324.00        Matches:          434
Percent Similarity:      99.77%        Conservative:       0
Best Local Similarity:   99.77%        Mismatches:         0
Query Match:             99.23%        Indels:             1
DB:                      11            Gaps:               0

US-09-607-745-2 (1-435) x US-09-776-191-71 (1-2079)

Qy    2  AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg    21
Db  217  GATCCTGCACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTCGCAAACCCCGT   276
Qy   22  IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuLeuSerLe   41
Db  277  ATCCCCATGGAGACCTTCAGAAGTGTGGGATCCCATCATCATCGCACTACTGAGCCT     336
Qy   41  uAlaSerIleIleIleValValLeuIleLysValIleLeuLeuAspLysTyrTyrPheLe   61
Db  337  GGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATAAATACTACTTCCT        396
Qy   61  uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCy   81
Db  397  CTGCGGCCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTG   456
Qy   81  sProLeuGlyAspGluGluHisCysValLysSerPheProGluGlyProAlaValAl     101
Db  457  TCCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCCTGCAGTGGC   516
Qy  101  aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr   121
Db  517  AGTCCGCCTCTCCAAGGACCGATCCACACTGCAGTGCTGGACTGCGCCACAGGGAACTG    576
Qy  121  pPheSerAlaCysPheAspAsnPheThrGluAlaAlaGluThrAlaGlyArgGlnMe     141
Db  577  GTTCTCTGCCTGTTTCGACAACTTCACAGAGCTCTCGCTAGGACAGCCTGTAGGCAGAT    636
Qy  141  tGlyTyrSerSerLysProThrPheArgAlaValAlaGluIleGlyProAspGlnAspLeuAs 161
Db  637  GGGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA   696
Qy  161  pValValGluIleThrGluAsnSerGlnLeuAsnSerGlyMetArgAsnSerSerGlyProCy 181
Db  697  TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGATCGGGAACTCAAGTGGCCCTG     756
Qy  181  sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuGlySerThrPr 201
Db  757  TCTCTCAGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGAAGAGCCTGAGAGACCCC   816
Qy  201  oArgValValGlyGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGl     221
Db  817  CCGTGTGGTGGGTGGGGAGGAGGAGCCCTCTGTGGATTCTTGGCCTTGGCAGTGCAGCATCCA 876
Qy  221  nTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl   241
Db  877  GTACGACAAACAGCACGTCTGTGGAGGAGCATCCTGGACCCCCACTGGGTCCTCACGGC   936
Qy  241  aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs   261
Db  937  AGCCCACTTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGA   996
Qy  261  pLysLeuGlySerPheProSerLeuAlaValAlaAlaLysIleIleIleGluPheAsnPr   281
Db  997  CAAACTGGGACGAGTCCCATCCCAGCCTGTGCCAAGATCATCATTGAATTCAAACCC     1056
Qy  281  oMetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheProLeuThrPheSe     301
Db 1057  CATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTC  1116
Qy  301  rGlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPr     321
Db 1117  AGGCACAGTCAGGCCCATCTGCTCGCCCTTCTTTGATGAGGAGCTCACTCCCAGCCACCCC 1176
Qy  321  oLeuTrpIleIleGlyIleGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLe   341
Db 1177  ACTCTGGATCATTGGGATGGGGCTTTACGGACAGCAGAATGGAGGAAGAGTGTCTGACATACT 1236
Qy  341  uLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspSerAlaTyrGl   361
Db 1237  GCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCA  1296
Qy  361  nGlyGluValThrGluLysMetMetCysAlaGlyIleIleProGluGlyValAspThrCy   381
Db 1297  GGGGGAAGTCACCGAGAAGATGATGTGCGCAGGCATCCCGGAAGGGGGTGTGGACACCTG  1356
Qy  381  sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIl   401
Db 1357  CCAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCAT  1416
Qy  401  eValSerTrpGlyTyrGlyCysGlyAspProSerThrProGlyValTyrThrLysValSe   421
Db 1417  CGTTAGCTGGGGCTATGGCTGCGGGGACCCCAGCACCCCAGGAGTATACCAAGGTCTC    1476
Qy  421  rAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1477  AGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1519
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RESULT 7
US-09-776-191-71

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CJA8 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)..(1522)
; OTHER INFORMATION: human CGA8
US-10-264-820-22

Alignment Scores:
Pred. No.:                4.03e-281        Length:        2079
Score:                   2324.00           Matches:        434
Percent Similarity:        99.77%          Conservative:     0
Best Local Similarity:     99.77%          Mismatches:       0
Query Match:               99.23%          Indels:           1
DB:                                        Gaps:             0
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US-09-607-745-2 (1-435) x US-10-264-820-22 (1-2079)

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Qy      2 AspProAspSerAspGlnProLeuAsnSerLeuAsnAspValLysProLeuArgLysProArg  21
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCTGGCCAAACCCCGT      276

Qy     22 IleProMetGluThrPheArgLys-ValGlyIlePheIleProIleIleIleAlaLeuLeuSerLe  41
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 ATCCCCATGGAGACCTTCAGAAAGTGGGATCCCATCATCATAGCACTACTGAGCCT          336

Qy     41 uAlaSerIleIleIleValValLeuuIleLysValIleLeuLeuAspLysTyrTyrPheLe  61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GGCGGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCCT    396

Qy     61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysGlyAspGlyLeuLeuAspCy  81
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 CTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGCTGACTG        456

Qy     81 sProLeuGlyGluAspGluHisCysValLysSerPheProGluProAlaValAl 101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 TCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGC     516

Qy    101 aValArgLeuAsnSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnThr 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 AGTCCGGCTCTTCCAAGGACCGATCACACTCCAGGTGCTGGACTCGGCCACAGGGAACTG     576

Qy    121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaLeuThrAlaCysArgGlnMe 141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGAT     636

Qy    141 tGlyTyrSerSerProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 GGGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAGATTGGCCCAGGATCTGA          696

Qy    161 pValValGluIleThrGluAsnSerGlnLeuArgMetArgAsnSerGlyProCy 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 TGTTGTTGAAATCACCAGAAACAGCCAGGAGCTTCGCATGCGAAACTCAAGTGGGCCCTG     756

Qy    181 sLeuSerGlyValGlyGluHisSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr 201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 TCTCTCAGGGTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCC     816

Qy    201 oArgValValGlyValGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGl 221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 CCGTGTGGTGGGTGGGGAGGAGGCCTCTGGCCTTGGCCTTGGCAGTCAGCATCCA         876

Qy    221 nTyrAspLysGlnHisValCysGlyGlySerIleLeuAspHisTrpValLeuThrAl 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 GTACGACAAACAGCACGTGTGTGGAGGGAGCATCCTGGACCCCACGGTCCTCACGGC       936

Qy    241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 AGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGTTCAGA     996

Qy    261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluProAsnPr 281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 CAAACTGGGAGCAGCTTCCCATCCTGGCTGTGGCCAAGATCATCATTGAAATTCAACCC    1056

Qy    281 oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 CATGTACCCCAAAGACAATGACATAGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTC    1116

Qy    301 rGlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPr 321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 AGGCACAGTCAGGCCCATCTGTCTGCCCTTCGATGAGGAGCTCACTCCAGCCACCCC     1176

Qy    321 oLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLe 341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 ACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACT    1236

Qy    341 uLeuGlnAlaSerValGlnValIleAspAspArgCysAsnAlaAspAspAlaTyrGl 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 GCTGCAGGCGTCAGTCCAGGTCATTGACGACAGAATGCAATGCAGACGATGCGTACCA     1296

Qy    361 nGlyLysValGluLysMetCysAlaGlyTyrIleProGluGlyGlyValAspAspThrCy 381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 GGGGAAGTCACCGAAGAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTG     1356

Qy    381 sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerSerGlnTrpHisValValGlyIl 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 CCAGGGTGACAGTGGTGGCCCCTGATGTACCAGTGCCATGTGGTGGGCAT             1416

Qy    401 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrArgLysValSe 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 CGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTC    1476

Qy    421 rAlaTyrLeuAsnTrpIleTyrAsnValTrpAsnValTrpLysAlaGluLeu             435
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1477 AGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG                    1519
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RESULT 8
US-10-264-820-22
; Sequence 22, Application US/10264820
; Publication No. US20030108926A1
; GENERAL INFORMATION:
;   APPLICANT: Eos Biotechnology, Inc.
;   TITLE OF INVENTION: No.US20030108926A1e1 Methods of Diagnosing Colorectal Cancer,
;   TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
;   TITLE OF INVENTION: Cancer Modulators
;   FILE REFERENCE: 018501-0061411US
;   CURRENT APPLICATION NUMBER: US/10/264,820
;   CURRENT FILING DATE: 2003-02-20
;   PRIOR APPLICATION NUMBER: US 09/268,866
;   PRIOR FILING DATE: 1999-03-15
;   PRIOR APPLICATION NUMBER: US 09/435,945
;   PRIOR FILING DATE: 1999-11-09
;   PRIOR APPLICATION NUMBER: US 09/436,983
;   PRIOR FILING DATE: 1999-11-09
;   PRIOR APPLICATION NUMBER: US 09/450,857
;   PRIOR FILING DATE: 1999-11-29
;   PRIOR APPLICATION NUMBER: US 09/453,850
;   PRIOR FILING DATE: 1999-12-02
;   PRIOR APPLICATION NUMBER: US 09/493,444
;   PRIOR FILING DATE: 2000-01-28
;   PRIOR APPLICATION NUMBER: US 09/525,993
;   PRIOR FILING DATE: 2000-03-15
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2079

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Qy      2  AspProSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg        21
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Db    217  GATCCTGACAGTGATCAACCTCGAAGACAGCCTCGATGTCAAACCCTGCGCAAACCCGT       276

Qy     22  IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaIleAlaLeuSerLe        41
           ||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db    277  ATCCCCATGGAGACCTTCAGAAAGTGTGGGGATCCCCATCATCATCAGCACTACTGAGCCT      336

Qy     41  uAlaSerIleIleIleValValLeuLeuLysValIleLeuAspTyrTyrPheLe        61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337  GGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTCTGGATAATATACTTCTCCT      396

Qy     61  uCysGlyGlnProLeuHisPheIleProArgLysGlyGlnLeuCysAspGlyGluLeuAspCy        81
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397  CTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCCTGTGTGACGGAGAGCTGGACTG      456

Qy     81  sProLeuGlyGluAspHisCysValLysSerPheGlnLysProAlaValAl       101
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457  TCCCCTTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCCTGGCAGTGGC      516

Qy    101  aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnThr       121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517  AGTTCGGCTTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAACTG      576

Qy    121  pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe       141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577  GTTCTCTGCCTGTTTTGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGAT      636

Qy    141  tGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs       161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637  GGGCTACAGCAGCAAACCCACCTTTCAGAGCTGTGGAGATTGGCCCAGACCAGATCTGGA      696

Qy    161  pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCy       181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697  TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTG      756

Qy    181  sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr       201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757  TCTCTCAGGTCCCCTGGCTCCCTGCACTGTTGCCTGTGGGAAGAGCCTGAAGACCCC       816

Qy    201  oArgValValGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGl       221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817  CCGTGTGTGTGGGTGGGGAGGAGGCCTCGTGGACCATTCTGGCCTGGCAGGTCAGCATCCA      876

Qy    221  nTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl       241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877  GTACGACAAAACAGCACGTCTGTGGAGGAGCATCCTGGACCCCCACTGGGTCCTCACGGC      936

Qy    241  aAlaHisCysPheArgLysHisThrAspAsnPheAsnTrpValArgAlaGlySerAs       261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937  AGCCCACTGCTTCCAGAAACATACCGATGTGTTCAACTGGGTGCGGGCAGGCTCAGA      996

Qy    261  pLysLeuGlySerPheProSerLeuAlaValAlaLalAlaIleIleIleGluProAsnPr       281
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997  CAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCC      1056

Qy    281  oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnInPheProLeuThrPheSe       301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057  CATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTC      1116

Qy    301  rGlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPr       321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117  AGGCACAGTGCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCC      1176

Qy    321  oLeuTrpIleIleGlyTrpGlyTyrThrLysGlnAsnGlyLyLysMetSerAspIleLe       341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177  ACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGAGATGTCTGACATACT      1236

Qy    341  uLeuGlnAlaSerValGlnValIleLeuAspSerThrArgCysAsnAlaAspAlaTyrGl       361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237  GCTGCAGGCGTCAGTCAGGTCATTGACAGCACCACGTGCAATGCAGATGCGTACCA      1296
```

(Second portion — rotated text at bottom, columns continuing)

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Db    997  CAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCC      1056
Qy    281  oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnInPheProLeuThrPheSe       301
Db   1057  CATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTC      1116
Qy    301  rGlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPr       321
Db   1117  AGGCACAGTGCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCC      1176
Qy    321  oLeuTrpIleIleGlyTrpGlyTyrThrLysGlnAsnGlyLyLysMetSerAspIleLe       341
Db   1177  ACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGAGATGTCTGACATACT      1236
Qy    341  uLeuGlnAlaSerValGlnValIleLeuAspSerThrArgCysAsnAlaAspAlaTyrGl       361
Db   1237  GCTGCAGGCGTCAGTCAGGTCATTGACAGCACCACGTGCAATGCAGATGCGTACCA      1296
Qy    361  nGlyValThrGluLysMetCysAlaGlyTyrIleProGlyGlyValGlyValValAspThrGly       381
Db   1297  GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTG      1356
Qy    381  sGlnAspAspSerGlySerGlyValPheGlyLeuMetTyrGlnSerAspSerTrpHisValValGlyIl       401
Db   1357  CCAGGGTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCAT      1416
Qy    401  eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe       421
Db   1417  CGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTC      1476
Qy    421  rAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGlnLeu       435
Db   1477  AGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG      1519
```

RESULT 9

US-10-254-289-1

; Sequence 1, Application US/10254289
; Publication No. US20030118509A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/10/254,289
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/656,002
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-254-289-1

Alignment Scores:

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Pred. No.:             4.0e-281         Length:         2079
Score:                 2324.00          Matches:        434
Percent Similarity:    99.77%           Conservative:   0
Best Local Similarity: 99.77%           Mismatches:     0
Query Match:           99.23%           Indels:         1
                       14                Gaps:           0
```

US-09-607-745-2 (1-435) x US-10-254-289-1 (1-2079)

```
Qy   361  nGlyGluValThrGluLysMetMetCysAlaAlaGlyIleProGluGlyGlyValAspThrCy  381
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1297  GGGGGAAGTCACCGAGAAGATGATGTGTGCAGCATCCCGGAAGGGGGTGTGGACACCTG  1356

Qy   381  sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspTrpGlnSerAspTrpHisValValGlyIl  401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1357  CCAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGCCATGGTGGTGGGCAT  1416

Qy   401  eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe  421
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1417  CGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTC  1476

Qy   421  rAlaTyrLeuAsnTrpIleTyrAsnValTrpAsnValTrpLysAlaGluLeu  435
               ||||||||||||||||||||||||||||||||||
Db  1477  AGCCTATCTCAACTGATCTACAATGTCTGGAAGGCTGAGCTG  1519


RESULT 10
US-09-776-191-3
; Sequence 3, Application US/09776191
; Publication No. US20030111168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE:  2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 3
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo Sapien
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(1574)
; OTHER INFORMATION: DNA sequence encoding a transmembrane serine
; OTHER INFORMATION: protease (MTSP3) protein
US-09-776-191-3

Alignment Scores:
Pred. No.:                 1.79e-280    Length:             2137
Score:                     2319.00      Matches:            432
Percent Similarity:        99.54%       Conservative:       0
Best Local Similarity:     99.54%       Mismatches:         2
Query Match:               99.02%       Indels:             0
DB:                        11           Gaps:               0

US-09-607-745-2 (1-435) x US-09-776-191-3 (1-2137)
```

```
Qy     1  AspProSerAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg  21
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2  GATCCTGACAGTGACGATCAACCTCTGAACAGCCTGGACGTGAAACAGCCCCTGCGGAAACCCCGT  329

Qy    22  IleProMetGluThrPheArgLysValGlyIleProIleIleAlaLeuLeuSerLeu  41
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330  ATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCGCACTACTGAGCCTG  389

Qy    42  AlaSerIleIleIleValValLeuIleLeuLysAspLysTyrPheLeu  61
               |||||||||||||||||||||||||||||||||||||||||||||
Db   390  GCGAGTATCATCATTGTGGTGCTCCTCATCAAGGTGCTGGTCTGGATAAATACTACTTCCTC  449

Qy    62  CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyLeuAspCys  81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   450  TGCGGGGACCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGCTGGACTGT  509

Qy    82  ProLeuGlyAspGluHisCysValLysSerValPheProGluGlyProAlaValAla  101
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510  CCCTTGGGGGAGGACGAGCACTGTGTCAAGAGCGTTCCCCAAGGGCCTGCAGTGGCA  569

Qy   102  ValAlaArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp  121
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570  GTCGCGCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACAGCGCCACAGGGAACTGG  629

Qy   122  PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet  141
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630  TTCTCTGCGTTTGACAACTTCACAGAAGCTCTCGCTGAGACAGCGTGTAGGCAGATG  689

Qy   142  GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp  161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690  GGCTACAGCAGCAAACCCACCTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGAT  749

Qy   162  ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys  181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750  GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGT  809

Qy   182  LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysLeuAlaCysSerLeuLysThrPro  201
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810  CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGAAGAGCCTGAAGACCCCC  869

Qy   202  ArgValValGlyGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGln  221
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870  CGTGTGGTGGGTGGGGAAGCGAGTGTGGATTCCTGGCCTTGGCAGGTCAGCATCCAG  929

Qy   222  TyrAspLysLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla  241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930  TACGACATACAGCACAGTGTGTGGAGGAGCATCCTGAACCCCCACTGGGTCCTCACGGCA  989

Qy   242  AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp  261
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990  GCCCACTCCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCCGGCTCAGAC  1049

Qy   262  LysLeuLeuGlySerPheProSerLeuAlaValAlaLysTyrIleIleIleIleGluProAsnPro  281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1050  AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC  1109

Qy   282  MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrPheSer  301
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1110  ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGCCCCTCACTTTCTCA  1169

Qy   302  GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro  321
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1170  GGCACAGTGCAGGCTCATCGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA  1229

Qy   322  LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu  341
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1230  CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG  1289

Qy   342  LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln  361
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1290  CTGCAGGCGTCAGTGCAGGTCATTGACAGCACACGTGCAATGCAGCGATGCTACCAG  1349

Qy   362  GlyGluValThrGluLysMetMetCysAlaAlaGlyIleIleProGluGluGlyValValAspThrCys  381
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1350  GGGGAAGTCACCGAGAAGATGATGTGTGCAGGGCATCCCGGAAGGGGGTGTGGACACCTGC  1409

Qy   382  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspTrpHisValValGlyIle  401
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1410  CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC  1469

Qy   402  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer  421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db
```

```
Db   1470 GTTAGCTGGGCTATGGCTGCGGGGGCCCGAGGAGCACCCCAGGAGTATACACCAAGGTCTCA 1529

Qy    422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
          AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu
Db   1530 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1571


RESULT 11
US-09-888-257A-2
; Sequence 2, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Hillan,Kenneth J.
;   APPLICANT: Polakis,Paul
;   APPLICANT: Smith,Victoria
;   APPLICANT: Wood,William I.
;   APPLICANT: Wu,Thomas D.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;   TITLE OF INVENTION: TREATMENT OF TUMOR
;   FILE REFERENCE: P5002R1
;   CURRENT APPLICATION NUMBER: US/09/888,257A
;   CURRENT FILING DATE: 2002-04-30
;   PRIOR APPLICATION NUMBER: US 60/063,540
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: US 60/089,653
;   PRIOR FILING DATE: 1998-06-17
;   PRIOR APPLICATION NUMBER: US 60/099,792
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: US 60/103,678
;   PRIOR FILING DATE: 1998-10-08
;   PRIOR APPLICATION NUMBER: US 60/235,451
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: PCT/US99/12252
;   PRIOR FILING DATE: 1999-06-02
;   PRIOR APPLICATION NUMBER: PCT/US99/20111
;   PRIOR FILING DATE: 1999-09-01
;   PRIOR APPLICATION NUMBER: PCT/US00/04342
;   PRIOR FILING DATE: 2000-02-18
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: 2000-03-02
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: 2000-03-30
;   PRIOR APPLICATION NUMBER: PCT/US00/23328
;   PRIOR FILING DATE: 2000-08-24
;   PRIOR APPLICATION NUMBER: PCT/US00/32678
;   PRIOR FILING DATE: 2000-12-01
;   PRIOR APPLICATION NUMBER: PCT/US01/06520
;   PRIOR FILING DATE: 2001-02-28
;   PRIOR APPLICATION NUMBER: PCT/US01/06666
;   PRIOR FILING DATE: 2001-03-01
;   NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
;   LENGTH: 2063
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-888-257A-2

Alignment Scores:
Pred. No.:              8.51e-278   Length:         2063
Score:                  2297.50     Matches:        429
Percent Similarity:     98.85%      Conservative:   0
Best Local Similarity:  98.85%      Mismatches:     0
Query Match:            98.10%      Indels:         5
                                    Gaps:           1

US-09-607-745-2 (1-435) x US-09-888-257A-2 (1-2063)

Qy      2 AspProAspSerAspGlnProLeuAsnSerLeuAsnValLysProLeuAspValLysProArg 21
          AspProAspSerAspGlnProLeuAsnSerLeuAsnValLysProLeuAspValLysProArg
Db    219 GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGGCCAAACCCCGT 278
```

(continuation of alignment — query/subject pairs)

```
Qy     22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu 41
          IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu
Db    279 ATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTG 338

Qy     42 AlaSerIleIleValValLeuLeuLysValIleLeuLeuLysLysAspLysTyrTyrPheLeu 61
          AlaSerIleIleValValLeuLeuLysValIleLeuLeuLysLysAspLysTyrTyrPheLeu
Db    339 GCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCCTC 398

Qy     62 CysGlyGlnProLeuHisPheProArgLysGlnLeuCysAspGlyLeuAspCys 81
          CysGlyGlnProLeuHisPheProArgLysGlnLeuCysAspGlyLeuAspCys
Db    399 TGCGGGCAGCCCTCCCACTTCATCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGT 458

Qy     82 ProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAla 101
          ProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAla
Db    459 CCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA 518

Qy    102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
          ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp
Db    519 GTCCGGCCCTCTCAAGGACCGATCACACTGCAGGTGCTGGACTCGGCCACCAGGGAACTGG 578

Qy    122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
          PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet
Db    579 TTCTCTGCCTGTTTCGACAACTTCACAGAGCTCCGCTGAGACAGCTGTAGGCAGATG 638

Qy    142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProGlnAspLeuAsp 161
          GlyTyrSerSerLysProThrPheArgAlaValGlu      ProGlnAspLeuAsp
Db    639 GGCTACAGC----------AGAGCTGTGGAGATTGGCCCAGGACCAGGATCTGGAT 683

Qy    162 ValValGluThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCys 181
          ValValGluThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCys
Db    684 GTTGTTGAAACTGAAAATAGCCAGAGCTTCGCATGCGAACTCAAGTGGGCCCTGT 743

Qy    182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
          LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro
Db    744 CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCC 803

Qy    202 ArgValValGlyGlyGluGluValAlaSerValAspSerTrpTrpGlnValSerIleGln 221
          ArgValValGlyGlyGluGluValAlaSerValAspSerTrpTrpGlnValSerIleGln
Db    804 CGTGTGTGGGGTGGGGAGGAGGTCGCTTCTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 863

Qy    222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
          TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla
Db    864 TACGACAAACAGCACGTCTGTGGAGGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

Qy    242 AlaHisCysPheArgGlyHisThrAspProSerValPheAsnTrpLysValArgAlaGlySerAsp 261
          AlaHisCysPheArgGlyHisThrAspProSerValPheAsnTrpLysValArgAlaGlySerAsp
Db    924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy    262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluProAsnPro 281
          LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluProAsnPro
Db    984 AAACTGGGCAGCTTCCCATCCCTGGCCGTGGCCAAGATCATCATTGAATTCAACCCC 1043

Qy    282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrProSer 301
          MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrProSer
Db   1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103

Qy    302 GlyThrValArgProIleCysLeuProPheGluProGluThrPro 321
          GlyThrValArgProIleCysLeuProPheGluProGluThrPro
Db   1104 GGCACAGTGAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy    322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
          LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu
Db   1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG 1223

Qy    342 LeuGlnAlaSerValGlnValIleLeuAspSerThrArgCysAsnAlaAspAlaTyrGln 361
          LeuGlnAlaSerValGlnValIleLeuAspSerThrArgCysAsnAlaAspAlaTyrGln
Db   1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGATGCGTACCAG 1283

Qy    362 GlyGluValThrGluLysProMetCysAlaGlyIleLeuProGluGlyGlyValAlaAspThrCys 381
          GlyGluValThrGluLysProMetCysAlaGlyIleLeuProGluGlyGlyValAlaAspThrCys
Db   1284 GGGGAAGTCACCGAGAAGAGATGATGTGTGCAGGCATCCTGCCCGAAGGGGGTGTGGACACCTGC 1343
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Qy    382  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344  CAGGGTGACAGTGGTGGGGCCCCTGAGTTACCAATCTGACCAGTGGCATGTGGTGGGCATC 1403

Qy    402  ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404  GTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy    422  AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
           ||||||||||||||||||||||||||||||||||||||
Db   1464  GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505


RESULT 12
US-09-946-374-274
; Sequence 274, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
;    APPLICANT: Baker, Kevin P.
;    APPLICANT: Botstein, David
;    APPLICANT: Desnoyers, Luc
;    APPLICANT: Eaton, Dan L.
;    APPLICANT: Ferrara, Napoleone
;    APPLICANT: Fong, Sherman
;    APPLICANT: Gao, Wei-Qiang
;    APPLICANT: Goddard, Audrey
;    APPLICANT: Godowski, Paul J.
;    APPLICANT: Grimaldi, Christopher J.
;    APPLICANT: Gurney, Austin L.
;    APPLICANT: Hillan, Kenneth J.
;    APPLICANT: Pan, James
;    APPLICANT: Paoni, Nicholas F.
;    APPLICANT: Roy, Margaret Ann
;    APPLICANT: Smith, Victoria
;    APPLICANT: Stewart, Timothy A.
;    APPLICANT: Tumas, Daniel
;    APPLICANT: Watanabe, Colin K.
;    APPLICANT: Williams, P. Mickey
;    APPLICANT: Wood, William I.
;    TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;    TITLE OF INVENTION: Acids Encoding the Same
;    FILE REFERENCE: P2830P1C1
;    CURRENT APPLICATION NUMBER: US/09/946,374
;    CURRENT FILING DATE:  2001-09-04
;    PRIOR APPLICATION NUMBER: 60/098716
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098723
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098749
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098750
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098803
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/098821
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/098843
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/099536
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099596
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099598
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099602
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099642
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099741
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099754
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099763
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099792
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099808
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099812
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099815
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099816
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/100385
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100388
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100390
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100584
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100627
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100661
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100662
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100664
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100683
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100684
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100710
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100711
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100848
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100849
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/100919
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100930
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/101014
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/101068
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/101071
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/101279
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/101471
;    PRIOR FILING DATE: 1998-09-22
;    PRIOR APPLICATION NUMBER: 60/101472
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101474
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101475
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101476
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101477
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101479
;    PRIOR FILING DATE: 1998-09-23
;    PRIOR APPLICATION NUMBER: 60/101738
;    PRIOR FILING DATE: 1998-09-24
;    PRIOR APPLICATION NUMBER: 60/101741
;    PRIOR FILING DATE: 1998-09-24
;    PRIOR APPLICATION NUMBER: 60/101743
;    PRIOR FILING DATE: 1998-09-24
;    PRIOR APPLICATION NUMBER: 60/101915
;    PRIOR FILING DATE: 1998-09-24
;    PRIOR APPLICATION NUMBER: 60/101916
;    PRIOR FILING DATE: 1998-09-24
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Best Local Similarity:   98.85%          Mismatches:   0
Query Match:             98.10%          Indels:       5
DB:                                      Gaps:         1

US-09-607-745-2 (1-435) x US-09-946-374-274 (1-2063)

Qy    2  AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg       21
Db  219  GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGGCAAACCCCGT      278

Qy   22  IleProMetGluThrPheArgGlyValGlyIleProIleIleIleAlaLeuLeuSerLeu       41
Db  279  ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGCCTG      338

Qy   42  AlaSerIleIleIleValValLeuIleLeuLysValIleLeuLeuAspLysTyrTyrPheLeu     61
Db  339  GCGAGTATCATCATTGTGGTTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTC        398

Qy   62  CysGlyGlnProLeuHisPhePheProArgLysGlnLeuCysAspGlyGluLeuAspCys       81
Db  399  TGCGGGCAGCCCCTCCACTTCATCCCGAGAAGCAGCTGTGTGACGGAGAGCTGGACTGT      458

Qy   82  ProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAla         101
Db  459  CCCTTGGGGGAGGACGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA        518

Qy  102  ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyLysAsnTrp    121
Db  519  GTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAACTGG      578

Qy  122  PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet      141
Db  579  TTCTCTGCCTGTTTCGACAACTTCACAGAGGCTCTCGCTGAGACAGCCTGTAGGCAGATG      638

Qy  142  GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuuAsp     161
Db  639  GGCTACAGC------AGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGAT              683

Qy  162  ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCys        181
Db  684  GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGAACTCAAGTGGGCCCTGT      743

Qy  182  LeuSerGlySerLeuValSerLeuHisCysLeuuAlaCysGlyGlyLysSerLeuuLysSerThrPro  201
Db  744  CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGAGCCCC      803

Qy  202  ArgValValGlyGlyGluGluuAlaSerValAspSerTrpProTrpGlnValSerIleGln     221
Db  804  CGTGTGGTGGGTGGGGAGGAGGCCTCGGTTCTTGGCCTTGGCAGTCAGTCAGCATCCAG      863

Qy  222  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla      241
Db  864  TACGACAAACAGCACGTCTGTGGGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA      923

Qy  242  AlaHisCysPheArgLysHisThrAspValPheAsnValArgAlaGlySerAsp           261
Db  924  GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAGAGGTGCGGCAGGTCAGAC      983

Qy  262  LysLeuGlyLysSerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro   281
Db  984  AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTGAATTCAACCCC       1043

Qy  282  MetTyrProLysAspAsnAspIleAlaLeuuMetLysGluGlnPheProLeuuThrPheSer    301
Db 1044  ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA     1103

Qy  302  GlyThrValArgProIleCysLeuuProPhePheAspGluGluuThrProAlaThrPro      321
Db 1104  GGCACAGTGAGGCCCATCTGCTGCCCTTCTTTGATGAGGAAGATGTCTGACATACTG       1163

Qy  322  LeuTrpIleIleGlyTyrTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu   341
Db 1164  CTCTGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG      1223
```

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Alignment Scores:
Pred. No.:
Score:                8.51e-278       Length:         2063
                      2297.50         Matches:         429
Percent Similarity:   98.85%          Conservative:      0
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```
Qy    339 GCGAGTATCATCATTGTGGTTGTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCCTC 398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        ...

Qy     62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyLeuLeuAspCys 81
Qy    342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
Db   1224 CTGCAGGCCGTCAGTCCAGGTCATTGACAGCAGCACGGTGCAATGCGACGATGCGTACCAG 1283

Qy    399 TGCGGGGCAGCCCTCCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGCGTGGACTGT 458
Qy    362 GlyGluValThrGluLysMetCysAlaGlyIleLeuProGluGlyIleGlyValAspThrCys 381
Db   1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGGGATCATCCCGGAAGGGGTGTGGACACTG 1343

Qy    459 CCCTTGGGGAGGACGAGAGCACTGTGTCAAGAGCTTCCCGAAGAGGGCCTGCAGTGGCA 518
Qy    382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerArgAspIleWrpHisValValGlyIle 401
Db   1344 CAGGGTGACAGTGGTGGCCCCTGATGACCAGTGGCATGGCTGGTGGTGGGCATC 1403

Qy    102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
Qy    402 ValSerTrpIleTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
Db    519 GTCCGCCTCCTCCAAGGACCGATCCACACTGGAGGTGCTGGACTCGGCCACAGGGACTGG 578
Db   1404 GTTAGCTGGGGCTATGGCTGCGGGGGGCCCGAGCACCCCGAGAGTATACACCAAGGTCTCA 1463

Qy    122 PheSerLeuCysPheAspAsnPheThrGluAlaLeuGluThrAlaCysArgGlnMet 141
Qy    422 AlaTyrLeuAsnTrpIleTyrArgAsnValTrpLysValAlaGluLeu 435
Db    579 TTCTCTGCCTGTTTCGACAACTTCACAGAGGCTCTGCTGACAGCCTGAGGACAGATG 638
Db   1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGTGAAGCTGGAGCTG 1505

Qy    142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyTyrProAspGlnAspLeuAsp 161
Db    639 GGCTACAGC------------AGAGCTGTGGAGAATTGGCCCAGACCAGGATCTGGAT 683

RESULT 13
US-10-015-387A-274
; Sequence 274, Application US/10015387A
; Publication No. US2003135034A1
; GENERAL INFORMATION:
Qy    162 ValValGluIleThrGluAsnSerGlnHisLeuArgMetArgAsnSerSerGlyProCys 181
Db    684 GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGT 743

;  APPLICANT: Baker, Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
Qy    182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
Db    744 CTCTCAGGTCCCCTGGTCTCTCCCTGCCACTGTCTGGGAGAGCCTGAAGACCCCC 803

;  APPLICANT: Eaton, Dan 1.
;  APPLICANT: Ferrara, Napoleone
;  APPLICANT: Fong, Sherman
Qy    202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db    804 CGTGTGGTGGGTGGGGAGGGCCCTCTGTGGATTCTTGGCCTTGCCAGTGCAGCATCCAG 863

;  APPLICANT: Gao, Wei-Qiang
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Godowski, Paul J.
Qy    222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db    864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923

;  APPLICANT: Grimaldi, Christopher J.
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Hillan, Kenneth J.
Qy    242 AlaHisCysArgLysHisValPheAspValPheAsnTrpLysValArgAlaGlySerAsp 261
Db    924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983

;  APPLICANT: Pan, James
;  APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
Qy    262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluProAsnPro 281
Db    984 AAACTGGGCAGCTTCCCATCCTGGCTGTGGCCAAGATCATCATTATTGAATTCAACCCC 1043

; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
Qy    282 MetTyrProLysAspAsnAspIleAlaAlaLeuMetLysAsnLysLysGlnSerLeuGlnPheProLeuThrPheSer 301
Db   1044 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGTGCAGTTCCCACTCACTTTCTCA 1103

; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
Qy    302 GlyThrValArgProIleCysLeuProPhePheAspGluThrProAlaThrPro 321
; TYPE: DNA
; ORGANISM: Homo sapiens
Db   1104 GGCACAGTGCAGGCCCCATCTGTCTGCCCCTTCTTTGATGAGGAGACTCCACTCCAGCCACCCCCA 1163
US-10-015-387A-274

Alignment Scores:
Pred. No.:                                  Length:        2063
Score:             8.51e-278                Matches:       429
Percent Similarity: 98.85%                  Conservative:  0          Qy  322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
                   2297.50                  Mismatches:    0
Best Local Similarity: 98.85%               Indels:        5          Db 1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG 1223
Query Match:       98.10%                   Gaps:          1
DB:                12                                                 Qy  342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
                                                                     Db 1224 CTGCAGGCCGTCAGTCCAGGTCATTGACAGCAGCACGGTGCAATGCGACGATGCGTACCAG 1283

US-09-607-745-2 (1-435) x US-10-015-387A-274 (1-2063)

Qy      2 AspProGluSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21     Qy  362 GlyGluValThrGluLysMetCysAlaGlyIleLeuProGluGlyIleGlyValAspThrCys 381
                                                                     Db 1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGGGATCATCCCGGAAGGGGTGTGGACACTG 1343
Db    219 GATCCTGACAGTGATCAACCTCTGAACAGCCTCGACGTCAAACCCCGT 278

Qy     22 IleProMetGluThrPheArgLysValGlyIleProIleIleGluAlaLeuLeuSerLeu 41     Qy  382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerArgAspIleTrpHisValValGlyIle 401
Db    279 ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCGAGGCTGCTGCTCTCACTG 338   Db 1344 CAGGGTGACAGTGGTGGCCCCTGATGACCAGTACCAAATCTGACCAGTGGCATGTGGGCATC 1403

Qy     42 AlaSerIleIleIleValValLeuLeuLysLysValIleLeuAspLysTyrTyrPheLeu 61     Qy  402 ValSerTrpIleTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
                                                                     Db 1404 GTTAGCTGGGGCTATGGCTGCGGGGGGCCCGAGCACACCCCGAGAGTATACACCAAGGTCTCA 1463
```

```
Qy   422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
         ||||||||||||||||||||||||||||||||||||||||||
Db  1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
```

RESULT 14
US-10-063-735-111
; Sequence 111, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 111
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-735-111

Alignment Scores:
Pred. No.:   Length: 2063
Score: 8.51e-278   Matches: 429
Percent Similarity: 98.85%   Conservative: 0
Best Local Similarity: 98.85%   Mismatches: 0
Query Match: 98.10%   Indels: 5
DB: Gaps: 1

US-09-607-745-2 (1-435) x US-10-063-735-111 (1-2063)

```
Qy     2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   219 GATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCTGCGCAAACCCCGT 278
```

```
Qy    22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu 41
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   279 ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGCCTG 338
```

```
Qy    42 AlaSerIleIleIleValValLeuIleLysValIleLeuValIleLeuLysAspTyrTyrPheLeu 61
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   339 GCGAGTATCATCATCGTGGTTGTCCTCATCAAGGTATTCTGATAAATACTACTTCCTC 398
```

```
Qy    62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluCysAspCys 81
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   399 TGCGGGCAGCCTCTCCACTTCATCCCGAGAAGCAGCTGTGTGACGGAGAGCTGGACTGT 458
```

```
Qy    82 ProLeuGlyAspGluHisPheIleProGluGlyProGluGlyProAlaValAla 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   459 CCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA 518
```

```
Qy   102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerArgAlaThrGlyAsnTrp 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 GTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGCGGGCCACAGGGAACTGG 578
```

```
Qy   122 PheSerAlaCysPheAspAspAsnPheThrGluAlaLeuAlaThrAlaCysArgGlnMet 141
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   579 TTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTGCTAACAGCCTGTAGGCAGAGATG 638
```

```
Qy   142 GlyTyrSerSerProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
         |||||||||||||||||||||||||||||          ||||||||||||||||||
Db   639 GGCTACAGC----------------AGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGAT 683
```

RESULT 15
US-10-006-130A-274
; Sequence 274, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

```
Qy   162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGATGCCGCAACTCAAGTGGGCCCTGT 743
```

```
Qy   182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 CTCTCAGGTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCC 803
```

```
Qy   202 ArgValValGlyGluGlnAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CGTGTGTGGGTGGGGAGGAGGCCTCTGTGGATTCTGGCCTTGGCAGGTCAGCATCCAG 863
```

```
Qy   222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA 923
```

```
Qy   242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValAlaArgAlaGlySerAsp 261
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGGCGGCAGCCTCAGAC 983
```

```
Qy   262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 281
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 AAACTGGGCAGCTTCCCATCCCTGGCCGTGGCCAAGATCATCATCATTGAATTCAACCCC 1043
```

```
Qy   282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044 ATGTACCCCAAAGACAATGACATGCCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103
```

```
Qy   302 GlyThrValArgProIleCysLeuProGlnPhePheAspGluGluLeuThrProAlaThrPro 321
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
```

```
Qy   322 LeuTyrIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 341
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGAAGATGTCTGACATACTG 1223
```

```
Qy   342 LeuGlnAlaSerValGlnValIleAspSerAsnThrArgCysAsnAlaAspAspAlaTyrGln 361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCAACACACGGTGCAATGCAGACGATGCGTACCAG 1283
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Qy   362 GlyGluValThrGluLysMetCysAlaGlyTyrIleProGluGlyGlyValAspSerThrCys 381
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGGACACCTGC 1343
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Qy   382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
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Db  1344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC 1403
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Qy   402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValThrTyrThrLysValSer 421
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Db  1404 GTTAGCTGGGGCTATGGCTGCGGGGCCCCAGCACCCGGAGTATACACCAAGGTCTCA 1463
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Qy   422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
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Db  1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-274

Alignment Scores:
Pred. No.:
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Percent Similarity:      98.85%               Matches:        429
Best Local Similarity:   98.85%               Conservative:-  0
Query Match:             98.10%               Mismatches:     0
DB:                                           Indels:         5
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US-09-607-745-2 (1-435) x US-10-006-130A-274 (1-2063)

Qy     2  AspProAspSerGlnProLeuAsnSerLeuAspLysValLysProLeuArgLysProArg    21
Db   219  GATCCTGACAGTGATCAACCTCTGAACAGCCTGATGTCAAACCCTGCCAAACCCCGT   278

Qy    22  IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu    41
Db   279  ATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTG   338

Qy    42  AlaSerIleIleIleValValLeuIleLeuValIleLeuLysValLeuAspLysTyrPheLeu    61
Db   339  GCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATCTGGATAAATACTACTTCCTC   398

Qy    62  CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys    81
Db   399  TGCGGGCAGCCTCTCCACTTCATCCCGAGAAGCAGCAGCTGTGTGACGGAGAGCTGGACTGT   458

Qy    82  ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla   101
Db   459  CCCTTGGGGGAGGACCAGGAGCACTGTGTCAAGAGCTTCCCCGAGGGGCCTGCAGTGGCA   518

Qy   102  ValArgLeuSerLysAspArgSerThrLeuGlnLeuValLeuAspSerAlaThrGlyAsnTrp   121
Db   519  GTCCGGCCTTCCAAGGACCGATCCACACTCCAGCTCGTGCTGGACTCGGCCACAGGGAACTGG   578

Qy   122  PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet   141
Db   579  TTCTCTGCCTGTTTCGACAACTTCACAGAAGCCCTCGCTGAGACAGCCTGTAGGCAGATG   638

Qy   142  GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp   161
Db   639  GGCTACAGC---------AGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGAT   683

Qy   162  ValValGluIleThrGluAsnSerGlnGlnLeuLeuArgMetArgAsnSerSerGlyProCys   181
Db   684  GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAATGGGCCCTGT   743

Qy   182  LeuSerGlySerLeuHisCysLeuAlaCysSerLeuAlaSerLeuLysThrPro   201
Db   744  CTCTCAGGCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCC   803

Qy   202  ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln   221
Db   804  CGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG   863

Qy   222  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspGluProHisTrpValLeuThrAla   241
Db   864  TACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACGAGCCCCACTGGGTCCTCACGGCA   923

Qy   242  AlaHisCysPheArgLysHisThrAspValPheAsnTrpValArgAlaGlySerAsp   261
Db   924  GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGGTGCGGGCAGGCTCAGAC   983

Qy   262  LysLeuGlySerPheProSerLeuAlaAlaLysIleIleIleGluGluPheAsnPro   281
Db   984  AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC  1043

Qy   282  MetTyrProLysAspAsnAspIleAlaLeuMetLysGlnPheProLeuThrPheSer   301
Db  1044  ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA  1103

Qy   302  GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro   321
Db  1104  GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGACCTCACTCCAGCCACCCCA  1163

Qy   322  LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu   341
Db  1164  CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTG  1223

Qy   342  LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln   361
Db  1224  CTGCAGGCGTCAGTCCAGTCATTGACAGCACACGGTGCAATGCAGACCGATGCGTACCAG  1283

Qy   362  GlyGluValThrGluLysMetMetCysAlaGlyIleLeuProGluGlyGlyValAlaAspThrCys   381
Db  1284  GGGGAAGTCACCGAGAAGATGATGTGCGCAGGCATCCCGGAAGGGGGTGTGGACACCTGC  1343

Qy   382  GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspTrpTrpGlnValValGlyIle   401
Db  1344  CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGTGGCAGTGTGGGCATC  1403

Qy   402  ValSerTrpGlyTyrGlyCysGlyProSerThrProGlyValTyrThrLysValSer   421
Db  1404  GTTAGCTGGGGCTATGGCTGCGGGCCCAGCACCCCAGGAGTATACACCAAGGTCTCA  1463

Qy   422  AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu   435
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Job time : 422.82 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:30:15 ; Search time 83.7689 Seconds
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Perfect score: 2342
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Searched: 569978 seqs, 22069156 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-Q=/cgn2_1/USPTO_spool_p/US09607745/runat_01122003_160938_9959/app_query.fasta_1.1038
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Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2338	99.8	2038	3	US-09-008-271A-18	Sequence 18, Appli
2	2324	99.2	2079	4	US-09-656-002-1	Sequence 1, Appli
3	677.5	28.9	2479	3	US-09-342-749-29	Sequence 29, Appl
4	677.5	28.9	2479	4	US-09-691-840-29	Sequence 29, Appl
5	676.5	28.9	1479	3	US-09-342-749-1	Sequence 1, Appl
6	676.5	28.9	1479	4	US-09-691-840-1	Sequence 1, Appli
7	650.5	27.8	2413	3	US-09-518-046-1	Sequence 1, Appli
8	627	26.8	2544	3	US-09-518-046-3	Sequence 3, Appli
9	621.5	26.5	2416	3	US-09-261-416-1	Sequence 1, Appli
10	584.5	25.0	1783	3	US-09-510-738A-188	Sequence 188, App
11	584.5	25.0	1783	4	US-09-861-966-188	Sequence 188, App
12	584.5	25.0	2363	4	US-09-742-703-3	Sequence 3, Appli

13	580	24.8	1615	4	US-09-820-002-1	Sequence 1, Appli
14	578	24.7	1605	2	US-09-000-846-1	Sequence 1, Appli
15	576	24.6	1460	4	US-09-370-838-80	Sequence 80, Appl
16	576	24.6	1517	1	US-08-508-448C-15	Sequence 15, Appl
17	576	24.6	2790	4	US-09-370-838-79	Sequence 79, Appl
18	574	24.5	1462	4	US-09-370-838-55	Sequence 55, Appl
19	571	24.4	2581	5	US-08-200-900A-1	Sequence 1, Appli
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21	558.5	23.8	1077	3	US-08-807-151-2	Sequence 2, Appli
22	558.5	23.8	1077	4	US-09-478-957-2	Sequence 2, Appli
23	531.5	22.7	696	1	US-08-508-448C-24	Sequence 24, Appl
24	516.5	22.1	901	1	US-08-508-448C-9	Sequence 9, Appli
25	503.5	21.5	959	4	US-09-023-942A-25	Sequence 25, Appl
26	496	21.2	1613	4	US-09-387-375-1	Sequence 1, Appli
27	483	20.6	1100	4	US-09-023-942A-5	Sequence 5, Appli
28	478	20.4	1081	3	US-09-008-271A-15	Sequence 15, Appl
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33	463	19.8	3147	4	US-09-027-337-1	Sequence 1, Appli
34	463	19.8	3147	4	US-09-644-600-1	Sequence 1, Appli
35	463	19.8	3147	4	US-09-644-600-18	Sequence 18, Appl
36	462.5	19.7	980	4	US-09-023-942A-30	Sequence 30, Appl
37	462.5	19.7	1212	4	US-09-620-312D-431	Sequence 431, App
38	458.5	19.6	1130	4	US-09-387-375-8	Sequence 8, Appli
39	458	19.6	1739	2	US-08-681-151-2	Sequence 2, Appli
40	449.5	19.2	1165	4	US-09-023-942A-28	Sequence 28, Appl
41	445	19.0	933	4	US-09-023-942A-29	Sequence 29, Appl
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43	443	18.9	2296	1	US-07-750-080A-18	Sequence 18, Appli
44	443	18.9	2296	3	US-08-651-472-18	Sequence 18, Appl
45	443	18.9	2296	3	US-08-358-928-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-008-271A-18
; Sequence 18, Application US/09008271A
; Patent No. 6203979
   GENERAL INFORMATION:
      APPLICANT: Bandman, Olga
                 Hillman, Jennifer L.
                 Yue, Henry
                 Guegler, Karl J.
                 Corley, Neil C.
                 Tang, Tom Y.
                 Shah, Purvi
   TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
   NUMBER OF SEQUENCES: 24
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Incyte Pharmaceuticals, Inc.
      STREET: 3174 Porter Dr.
      CITY: Palo Alto
      STATE: CA
      COUNTRY: USA
      ZIP: 94304
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette
      COMPUTER: IBM Compatible
      OPERATING SYSTEM: DOS
      SOFTWARE: FastSEQ for Windows Version 2.0
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/008,271A
      FILING DATE: 16-Jan-1998
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: <Unknown>
      FILING DATE: <Unknown>
   ATTORNEY/AGENT INFORMATION:
      NAME: Mohan-Peterson, Sheela
      REGISTRATION NUMBER: 41,201
      REFERENCE/DOCKET NUMBER: PF-0458 US

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TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-855-0555
    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2038 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    IMMEDIATE SOURCE:
        LIBRARY: COLNNOT13
        CLONE: 1337018
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-008-271A-18
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Pred. No.:                      6.49e-244
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Query Match:                    99.83%
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Qy     41  LeuAlaSerIleIleIleIleValValLeuIleLysValIleLeuAspLysLysTyrPhe  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121  TrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln  140
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Qy    141  MetGlyTyrSerLysSerProThrPheArgAlaValGluIleGlyLysProAspGlnLeu  160
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Qy    181  CysLeuSerGlySerLeuValSerLeuHisCysGlyLeuAlaCysGlyLeuValSerThr  200
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Qy    221  GlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspGluProHisTrpValLeuThr  240
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Qy    261  AspLysLeuGlySerPheProSerLeuAlaLysIleIleIleIleGluPheAsn  280
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Db    980  GACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAAC  1039

Qy    281  ProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnProLeuThrPhe  300
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Qy    321  ProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIle  340
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Qy    341  LeuLeuGlnAlaSerValGlnValValIleAspSerThrArgCysAsnAlaAspAspAlaTyr  360
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Db   1220  CTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTAC  1279

Qy    361  GlnGlyGluValThrGluHisLysMetMetCysAlaGlyIleProGluGlyGlyValAspThr  380
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Qy    381  CysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGly  400
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; Sequence 1, Application US/09655002
; Patent No. 6455668
; GENERAL INFORMATION:
;   APPLICANT: Mack, David
;   APPLICANT: Gish, Kurt
;   APPLICANT: Wilson, Keith
;   TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, A1
;   TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
;   FILE REFERENCE: A-69108/DJB/JJD/AMS
;   CURRENT APPLICATION NUMBER: US/09/656,002
;   CURRENT FILING DATE: 2000-09-06
;   PRIOR APPLICATION NUMBER: US 09/525,993
;   PRIOR FILING DATE: 2000-03-15
;   PRIOR APPLICATION NUMBER: US 09/493,444
;   PRIOR FILING DATE: 2000-01-28
;   PRIOR APPLICATION NUMBER: PCT/US 00/07044
;   PRIOR FILING DATE: 2000-03-15
;   SOFTWARE: PatentIn version 3.0
;   NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
;   LENGTH: 2079
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-656-002-1
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Alignment Scores:
Pred. No.:                      2.22e-242
Score:                          2324.00
Percent Similarity:             99.77%
Best Local Similarity:          99.77%
Query Match:                    99.23%

Length:         2079
Matches:        434
Conservative:   0
Mismatches:     0
Indels:         1
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Length: 2038
Matches: 434
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

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DB:
                                        4                       Gaps:   0

US-09-607-745-2 (1-435) x US-09-656-002-1 (1-2079)

Qy      2 AspProAspSerGlnProLeuAsnSerLeuArgValLysProLeuArgLysProArg 21
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GATCCTGACAGTGATCAACCTTCGAACAGCCTGAGGTCAAACCCTGCCAAACCCCGT 276

Qy     22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuLeuSerLe 41
          ||||||||||||||||||||||||
Db    277 ATCCCCATGGAGACCTTCAGAAAGTGGGGAATCCCCATCATCATAGCACTACTGAGCCT 336

Qy     41 uAlaSerIleIleIleValValLeuIleLysLysValIlleLeuAspLysTyrTyrPheLe 61
          |||||||||||||||||||||||||||||||||
Db    337 GGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATAAAATACTACTTCCT 396

Qy     61 uCysGlyGlnProLeuHisProAsnSerPheIleProArgLysGlnLeuCysSerAspGlyLeuAspCy 81
          |||||||||||||||||||||||||||||||
Db    397 CTGCGGGGCAGCCCTCTCCACTTCATCCCGAGAGCAGCTGTGTGACGGAGAGCTGGACTG 456

Qy     81 sProLeuGlyGluAspGluHisGluCysValLysSerSerPheProGluGlyProAlaValAl 101
          ||||||||||||||||||||||||||||||||||
Db    457 TCCCTTGGGGGAGGACGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGC 516

Qy    101 aValAlaArgLeuSerLysAspArgSerThrLeuGlnAsnValAspAspSerAlaThrGlyAsnTr 121
          |||||||||||||||||||||||||||||||||
Db    517 AGTCGCGCCTCTCCAAGGACCGATCCACACTGCAGAGTGCTGGACTCCGGCCACAGGGAACTG 576

Qy    121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
          |||||||||||||||||||||||||||||||
Db    577 GTTCTCTGCCTGTTTCGACAACTTCACAGAAGCCTCTGGCAGACGCCTGTAGGCAGAT 636

Qy    141 tGlyTyrSerSerProThrPheArgAlaValGlulleGlyProAspGlnAspLeuAs 161
          ||||||||||||||||||||||||||||
Db    637 GGGCTACAGCAGCCCAACCCCACTTTCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA 696

Qy    161 pValValGlulleThrGluSerGlnGlnLeuAsnSerGlnLeuArgMetArgAsnSerGlyProCy 181
          ||||||||||||||||||||||||||||||
Db    697 TGTTGTTGAAATCACAGAAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAGTGGGCCCTG 756

Qy    181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysSerLeuLysSerThrPr 201
          ||||||||||||||||||||||||||||||||||
Db    757 TCTCTCAGGCTCCCCTGGTCTCTTCGCCTGTCTTGCCTGTGGAAGAGCCTGAAGACCCCC 816

Qy    201 oArgValAlaGlyGlyGlyGluAlaSerValAlaSerValAspSerArgTrpProTrpGlnValSerIleGl 221
          ||||||||||||||||||||||||||||||||||
Db    817 CCGTGTGGTGGGGTGGGGGAGGCCTCTGTGGCCTCTGTGGATTCTTCGCCAGGTCAGCATCCA 876

Qy    221 nTyrAspLysSerGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl 241
          ||||||||||||||||||||||||||||||||
Db    877 GTACGACAAAAGCAGCACGTCTGTGGAGGAGCATCCTGACCCCCACTGGGTCCTCACGGC 936

Qy    241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysTrpProLysAspAspAlaGlySerAs 261
          |||||||||||||||||||||||||||||||||
Db    937 AGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGTGGCCGAAGGGCCTGCAGA 996

Qy    261 pLeuGlyArgProIleCysLeuProAspGluPheAspSerLeuAlaAlaLysAlaAlaAlaValAlaArgLeuAsnPr 281
          |||||||||||||||||||||||||||||||||
Db    997 CAAACTGGGCAGTCCATCCCGCTGCTGCCAAGATCATCATTGAATTCAACCC 1056

Qy    281 oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
          |||||||||||||||||||||||||||||||||
Db   1057 CATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTC 1116

Qy    301 rGlyThrValArgProIleCysLeuProPheAspGluLeuThrProAlaThrPr 321
          ||||||||||||||||||||||||||||
Db   1117 AGGGACAGTCAGGCCCATCTGCTGCCCTTCTTTGATGAGCTCACTCCAGCCACCCC 1176

Qy    321 oLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLe 341
          ||||||||||||||||||||||||||||||||
Db   1177 ACTCTGGATCATTGGATGGGGCTTTACCAAGCAGAATGGAGGGAAGATGTCTGACATACT 1236

Qy    341 uLeuGlnAlaSerValGlnValIleIleAspSerThrArgCysAsnAlaAspAspTyrGl 361
          --------------------------
Db   1237 GCTGCAGGCGTCAGTCATTGTCATCAGCATTGACAGCACGCGGTGCAATGCAGACGATGCTACCA 1296
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Qy    361 nGlyGluValThrGlulysMetCysAlaGlyIleProGluGlyGlyValAspThrCy 381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTG 1356

Qy    381 sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerGlnThrTrpHisValGlyI 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 CCAGGGGGACAGTGGTGGGGCCCCTGATGTACCAATCTGACCAGTGGGTGGGCAT 1416

Qy    401 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe 421
          |||||||||||||||||||||||||||||||||
Db   1417 CGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTC 1476

Qy    421 rAlaTyrLeuAsnTrpIleTyrArgValTrpLysAlaGluLeu 435
          |||||||||||||||||||||||||||||
Db   1477 AGCCTATCTAACTGGATCTACAAATGTCTGGAAGGCTGAGCTG 1519
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```
RESULT 3
US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
;   APPLICANT: Wong, Alexander K.C.
;   APPLICANT: Tavtigian, Sean V.
;   APPLICANT: Teng, David H.-F.
;   APPLICANT: Myriad Genetics, Inc.
;   TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
;   FILE REFERENCE: 2318-202
;   CURRENT APPLICATION NUMBER: US/09/342,749
;   CURRENT FILING DATE: 1999-06-29
;   EARLIER APPLICATION NUMBER: US 60/091,044
;   EARLIER FILING DATE: 1998-06-29
;   NUMBER OF SEQ ID NOS: 33
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 2479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-342-749-29

  Alignment Scores:
  Pred. No.:                              Length:        2479
  Score:                  1.81e-63        Matches:        151
  Percent Similarity:     54.05%          Conservative:    56
  Best Local Similarity:  39.43%          Mismatches:     127
  Query Match:            28.93%          Indels:          49
  DB:                        3            Gaps:            13

US-09-607-745-2 (1-435) x US-09-342-749-29 (1-2479)

Qy     75 CysAspSerGlyLeuAspCysProLeuGlyGluHisGluCysValLysSerPhe 94
          ::: :    :
Db    453 TGTGATGGCGTGCACATGCCCCGCGGGGAGGACGAGAATCGGTGTGTTCGCCCTCTAC 512

Qy     95 ProGluGlyProAlaValAlaValAlaArgLeuSerLysAspArgSerThrLeuGlnAsnValLeu 114
          :::    ::
Db    513 -----GGACCA------------------------------AACTTCATCCTTCAGATGTAC 539

Qy    115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
          ::::
Db    540 TCATCTCAGAGAGGAAGTCCTGCACCCTGTGTCCAAGACAGACTACGGG 599

Qy    135 GluThrAlaCysArgGlnMetGlyTyrSerSerProThrPheArgAlaValGluIle 154
          :::    ::
Db    600 CGGGCGGCCTGCAGGACATGGGCTAT------AAGAATAATTTTACTCTAGCCAA-- 650

Qy    155 GlyProAspGlnAspLeuAspLeuValValGluIleThrGluSerGlnGlnLeuArgMet 174
          :::    ::
Db    651 ----------GGAATAGTGGATGACAGCACGCCGATCACCACAGCTTTATGAAACTG 692

Qy    175 ArgAsnSerGly------------------------------ProCysLeu 182
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-840-29

Alignment Scores:
Pred. No.:                                          Length:          2479
Score:                 1.81e-63                     Matches:          151
Percent Similarity:    54.05%                       Conservative:      56
Best Local Similarity: 39.43%                       Mismatches:       127
Query Match:           28.93%                       Indels:            49
DB:                                                 Gaps:              13


US-09-607-745-2 (1-435)  x  US-09-691-840-29 (1-2479)

Qy    75  CysAspGlyGluLeuAspGlyCysProLeuGlyLysGluHisCysValLysSerPhe    94
                 :::           |||||||||||||||||
Db   453  TGTGATGGCGTGTCACACTGCCCGGCGGGAGGACGAGAATCGTGTTCGCCCTAC      512

Qy    95  ProGluGlyProAlaValAlaAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu  114
               :::
Db   513  ------GGACCA                                 AACTTCATCCTTCAGATGTAC  539

Qy   115  AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla   134
Db   540  TCATCTCAGAGGAAGTCCTGGCACCCTGTGCCAAGACGACTGGAACGAGAACTACGGG   599

Qy   135  GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGlyIle  154
Db   600  CGGGCGGCCTGCAGGGACATGGCTAT------AAGAATAATTTTACTCTAGCCAA--    650

Qy   155  GlyProAspGlnAspLeuAspValAlaValGluIleThrGluAsnSerGlnLeuArgMet  174
             :::|::                   ::  :::
Db   651  ------GGAATAGTGATGATGACAGCGGATCCCACCCAGCTTTATGAAACTG        692

Qy   175  ArgAsnSerSerGly-                                       ProCysLeu  182
Db   693  AACACAAGTGCCGGCAATGTCGATATCTATAAAAACTCTATAAAAACTGTACCACAGTGATGCCTGTTCT  752

Qy   183  SerGlySerLeuValSerLeuHisCysGlyLysSerLeu------         Lys  199
             :::::|:|||||
Db   753  TCAAAAGCAGTGGTTTCTTTACGCTGTTTAGCCTGCGGGGTCAACTTGAACTCAAGCCGC  812

Qy   200  ThrProArgValValGlyGluGluAlaSerValAspSerTrpProTrpGlnValSer  219
             :|:||||
Db   813  CAGAGCAGGATCGTGGGCGGCGGTGAGAGCCGGCTCCCGGGGGCCTGGCCTGCAGGTCAGC  872

Qy   220  IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu  239
             :::
Db   873  CTGCACGTCCAGAACGTCCACGTGCGGAGGCTCCATCATCACCCCCGAGTGGATCGTG  932

Qy   240  ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla  258
             |||               ||    ::::::||
Db   933  ACAGCCGCCCACTGCTTCAGAAAACCTCTTAACATCATCATGGCATTGCG  992

Qy   259  GlySerAspLysGlySerPhe------                        ProSerLeuAlaValAlaLysIle  274
             ::  :|||
Db   993  GGGATTTTGAGA---CAATCTTTCATGTTCTATGGAGCCGGATACCAAGTACAAAAGTG  1049

Qy   275  IleIleIleGluPheAsnProMetTyr------                 ProLysAspAsnProIleAlaLeu  291
             ||           ::::
Db  1050  ATT------TCTCATCCAAATTATGACTCCAAGAACAATGACATTGCGCTG  1100

Qy   292  MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe  311
             |||:|
Db  1101  ATGAAGCTGCAGAAGCCTCGACTTTCAACGACCTAGTGAACGTGTCTCGCCCAAC  1160

Qy   312  PheAspGluGluThrProAlaThrProLeuIleIleGlyGlyThrPheThrLys  331
             |||||||
Db  1161  CCAGGCATGATGCTGCAGCCAGAACAGTCTGCTGGATTCCGGGTGGGGGCCACCGAG  1220

Qy   332  GlnAsnGlyGlyLysMetSerAspAlaIleLeuLeuGlnAlaSerValGlnValIleAspSer  351
             ||||         ::::::::||
Db  1221  GAGAAA---GGGAAGAACCTCAGAAGTGCTGCTCCAAGGTGCTTCTCATTGAGACA  1277

Qy   352  ThrArgCysAsnAlaAspAspAlaTyrArgGlnGlyValThrGluValThrGluLysMetMetCysAla  371
             :::::||
Db  1278  CAGAGATGCAACAGCAGAGATGTCATGACAACCTGGGTTGTTGGCCATGATCGTGCC  1337

Qy   372  GlyIleProGluGluValGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr  391
             ||||||||||
Db  1338  GGCTTCCTGCGAAACGTCGATTCTTGCCAGGGTGACAGTGGAGGGGCCTCTGGTCACT  1397

Qy   392  GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly  410
             :: ||||||
Db  1398  TCGAACAACAATATCTGGTGGCTAGAGGGATAGAGACGCTGGGGTTCTGGCGTGCCAAA  1457

Qy   411  ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal  430
             :||:::||
Db  1458  GCTTACAGCACCAGGAGTGTACGGAGAGTGATTATTCACGGACTGGATTTATCGACAA  1517

Qy   431  TrpLysAla  433
             |||
Db  1518  ATGAAGGCA  1526
```

RESULT 4
US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 6444419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749

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Qy  312  PheAspGluLeuThrProAlaThrProLeuThrPheIleIleGlyTrpGlyPheThrLys 331
Db 1161  CCAGGCATGATGCTGCAGCCAGAACAGCTCTGCTGGATTCCGGGTGGGGGCCACCGAG 1220

Qy  332  GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
Db 1221  GAGAAA--GGGAAGAGACCTCAGAAGTGCTGAACGTGCCAAGGTGCTTCTCATTGAGACA 1277

Qy  352  ThrArgCysAsnAlaAspAspAlaTyrGlnGlyGluValThrGlyLysMetMetCysAla 371
Db 1278  CAGAGATGCAACAGCAGACGATATGTCTATGACAACCAGCCATGATCTGTGCC 1337

Qy  372  GlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr 391
Db 1338  GGCTTCCTGCGAGGGGAACGTCGATTCTTGCCAGGGTGACAGTGGAGGGCCTCTGGTCACT 1397

Qy  392  GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyTyrGlyCysGlyGly 410
Db 1398  TCGAACAACAATATCTGGTGGCTGATAGGGGATACAAGCTGGGGTTCTGGCTGTGCCAAA 1457

Qy  411  ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal 430
Db 1458  GCTTACAGACAGCAGGAGTGTACGGAAGTGTATGGTATTCACGGACTGGATTTATCGACAA 1517

Qy  431  TrpLysAla 433
Db 1518  ATGAAGGCA 1526
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RESULT 5
US-09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to
; OTHER INFORMATION: Ile
; US-09-342-749-1

Alignment Scores:
Pred. No.:   Length: 1479
Score: 1.04e-63   Matches: 676.50
Percent Similarity: 53.91%   Conservative: 57
Best Local Similarity: 39.06%   Mismatches: 128
Query Match: 28.89%   Indels: 49
DB: 3   Gaps: 13

US-09-607-745-2 (1-435) x US-09-342-749-1 (1-1479)

```
Qy   75  CysAspSerGlyGluLeuAspCysProLeuGlyGluAspGluHisCysValLysSerPhe 94
             ||||||||   ||:      ::::
Db  397  TGTGATGGGCGTGTCACACTGCCCGGCGGGAGGACGAGAATCGGTCGTGTTCGCCTCTAC 456

Qy   95  ProGluGlyProAlaValAlaValAlaArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
         |||||                        |||||||||
Db  457  -----GGACCA--------------AACTTCATCCTTCAGGTGTAC 483

Qy  115  AspSerAlaThrGlyAsnTrpProSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
             :::                  |||||       :::::::
Db  484  TCATCTCAGAGAGAAGTCCTGGCACCCTGTGCCAAGACGACTGGAACGAGAACTACGGG 543

Qy  135  GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIle 154
             ||||||                :::::       ||
Db  544  CGGGGCGCCTGCGAGGGACATGGGCTAT------AAGAATAATTTTACTCTAGCCAA-- 594

Qy  155  GlyProAspGlnAspLeuThrValValGluIleThrGluAsnSerGlnGluLeuArgMet 174
             ::||:       :::    ::::::      :::::::::
Db  595  ------------GGAATAGTGGATGACAGCGGATCCACCAGCTTTATGAAAACTG 636

Qy  175  ArgAsnSerSerGly-------------------------------ProCysLeu 182
             ||:||||:
Db  637  AACACAAGTGCCGCAATGTCGAATATCATATAAAAAACTGTACCACAGTGATGCCTGTTCT 696

Qy  183  SerGlySerLeuValSerLeuHisCysSerLeuAlaCysGlyLysSerLeu-------Lys 199
             :::||:||:||||||  ||||||||||
Db  697  TCAAAGCAGTGTTTTCTTACGCTGTATAGCCTGGGGTCAACTGAACTCAAGCCGC 756

Qy  200  ThrProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSer 219
             |||||||||||  ||||||||||||||||
Db  757  CAGAGCAGGATCGTGGGCGGCGAGAGCGCCTCCCGGGGCCTGGCAGGTCAGC 816

Qy  220  IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu 239
             :::
Db      
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; FEATURE:

Db 817 CTGCACGTCCAGAAGCTCCACGTGTGCGGAGGCTCCATCATCACCCCGAGTGGATCGTG 876
Qy 240 ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla 258
         |||||||||||||::::   :::: |||
Db 877 ACAGCCGCCCACTGCGTGGAAAAACCTCTTAACAATCCATGGCATTGGACGGCATTTGCG 936
Qy 259 GlySerAspLysLeuGlySerPhe----------ProSerLeuAlaValAlaLysIle 274
         ||| ::: |||||||
Db 937 GGGATTTTGAGA--CAATCTTTCATGTTCTATGGAGCCGGATACCAAGTAGAAAAAGTG 993
Qy 275 IleIleIleGluPheAsnProMetTyr------ProLysAspAsnAspIleAlaLeu 291
         |||||||||||||::: |||
Db 994 ATT------TCTCATCCAAATTATGACTCCAAGACCAAGAACAATGACATTGCGCTG 1044
Qy 292 MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysSerLeuProPhe 311
         |||||||||||
Db 1045 ATGAAGCTGCAGAAGCCCTGACTTTCAACGACCTAGTGAAACCAGTGTGTCTGCCCAAC 1104
Qy 312 PheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLys 331
         ||||| |||||||||
Db 1105 CCAGGGATGATGCTGCAGCCAGAGAGCTCTGCTGATTTCCGGTGGGGGGCCACCGAG 1164
Qy 332 GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
         ::: ||:::||||
Db 1165 GAGAAA---GGGGAAGACCTCAGAGTGCTGCCCAAGGTGCTTCTCATTGAGACA 1221
Qy 352 ThrArgCysAsnAlaAspAspAlaTyrGlnGlyGluValThrGluLysMetCysAla 371
               ::||| |||
Db 1222 CAGAGATGCAACAGCAGATATGTCTATGACAACCTGATCACCACCGAGAAGATCTGTGCC 1281
Qy 372 GlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr 391
         |||:::|||||||||||||||||||
Db 1282 GGCTTCCTGCAGGGGAACGTCGATTCTTGCCAGGTGACAGTGGAGGGCCTCTGGTCACT 1341
Qy 392 GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly 410
         ::: :::::||| |||||||||||
Db 1342 TCGAAGAACAATATCTGGTGGCTGATAGGGGATACAAGCTGGGGTTCTGGCTGTGCCAAA 1401
Qy 411 ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal 430
         ||| ::: |||||||
Db 1402 GCTTACAGACCAGGAGTGTACGGGAGATGTGGTATTCACGGACTGGATTTATCGACCA 1461
Qy 431 TrpLysAlaGlu 434
         :::|||
Db 1462 ATGAGGGGCAGAC 1473

; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329.
; NAME/KEY: allele
; LOCATION: (478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
US-09-691-840-1

Alignment Scores:
Pred. No.:
Score: 676.50   Length: 1479
Percent Similarity: 53.91%   Matches: 150
Best Local Similarity: 39.06%   Conservative: 57
Query Match: 28.89%   Mismatches: 128
DB: 4   Indels: 49
                                                              Gaps: 13
                           1.04e-63

US-09-607-745-2 (1-435) x US-09-691-840-1 (1-1479)

Qy   75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluHisCysValLysSerPhe 94
         || ::   ::: |||||||:::
Db 397 TGTGATGGCGTGTCACACTGCCCCGCGCGGGGAGGACGAGAATCGGTGTGTTCGCCTAC 456
Qy   95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerLysGlnValLeu 114
         ||||||| :::
Db 457 ------GGACCA------AACTTCATCCTTCAGGTGTAC 483
Qy 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
         :::||| ||:::||
Db 484 TCATCTCAGAGGAGGAAGTCCTGGCACCCTGTGTGCCAAGACGACTGGAACGAGAACTACGGG 543
Qy 135 GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIle 154
         ||| ::: |||
Db 544 CGGGCGGCCTGCAGGGACATGGGCTAT-----AAGAATAATTTTTACTCTAGCCAA--- 594
Qy 155 GlyProAspGlnAspLeuAspValGlyIleThrGluAsnSerGlnGluLeuArgMet 174
         :::   ::::: |||
Db 595 ------------GGAATAGTGCATGAGCAGCGGATCCACCAGCTTTATGAAACTG 636
Qy 175 ArgAsnSerSerGly---------ProCysLeu 182
Db 637 AACACAAGTGCCGGCAATGTCGATATCTATAAAAAACTGTACCACCAGTGATGCCTGTTCT 696
Qy 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGlyGlyLysSerLeu------Lys 199

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

Alignment Scores:
Pred. No.:                                      Length:        2413
Score:                 650.50                   Matches:        157
Percent Similarity:    52.14%                   Conservative:    74
Best Local Similarity: 35.44%                   Mismatches:     149
Query Match:           27.78%                   Indels:          63
DB:                                             Gaps:            18

                       1.49e-60

US-09-607-745-2 (1-435) x US-09-518-046-1 (1-2413)
```

```
Qy  22  IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu   41
            ::|||  |::|||                 :::
Db 273  CTGCCATTTGAAGTTTTTCCCAATCATCGTCATTGGGATCATTGCATTG--------     323

Qy  42  AlaSerIleIleIleValValValLeuIleLysValIleLeuAsp--------LysTyr    58
                :: :::  ::
Db 324  ------ATATTAGCACTGGCATTGTCTGGCATCCATCACCTTCGACTGCTCAGGGAGTAC   377

Qy  59  ---------TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu      74
                    |||    :::      |||
Db 378  AGATGTCGCTCATCCTTTAAGTGT--------ATCGAGCTGATAACTCGA             419

Qy  75  CysAspGlyGluLeuAspCysProLeuGlyGluAspGluGlyGluGlyGlnHisCysValLysSerPhe  94
        ||||||                              ::
Db 420  TGTGACGGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACCGCTGT--           467

Qy  95  ProGluGlyProAlaAlaAlaValArgValAlaArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
                           |||||||||
Db 468  --------GTCCGGTGGCTGGTGGTCAGAATGCCGTCCTCCAGGTGTTC              506

Qy 115  AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla  134
                                ::|||
Db 507  ACAGCTGCT----TCGTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCA    560

Qy 135  GluThrAlaCysArgGlnMetGlyThrSerSer-----                        145
        ||||:|:|                |||
Db 561  AATGTTGCCTCGTGCCCAACTGGGTTCCCAACGTATGGAGCTGATAACCTCAGAGTG      620

Qy 146  ------LysProThrPheArgAlaValAlaValLeuGlyProAspGlnAspLeuAspAspVal 162
Db 621  AGCTCGCTCGAGGGGCAGTTCGGGAGGAGAGTTTGTGTCCATGGATCACCTCTTGCCAGAT   680

Qy 163  ValGluIleThrGluAsnSerGlnGlnLeuArgMetArgAsnSerGlyProCysLeu     182
                                ||:||
Db 681  GACAAGGTGACTGCATTACCACCTCAGTATATGTGAGGGAGGGA--------TGTGCC     731

Qy 183  SerGlySerLeuValSerLeuHisCysLeuAlaCysGly----LysSerLeuLysThrPro 201
        ||||||
Db 732  TCTGGCACGTGGTTACCTTGCAGTGCACAGCCTGTGGTCATAGAAGGGGTACAGCTCA    791

Qy 202  ArgValValGlyGlyGluGluValAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
        ||| ||
Db 792  CGCATCGTGGGTGGAAACATGTCCTTGCTCTCCGAGTGCCCTGGCCAGCCCAGCCTTCAG   851

Qy 222  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla  241
                    :::    :
Db 852  TTCCAGGGTACCACCTGTCGGGGGCTCTGTCATCACGCCCCTGGATCATCACTGCT      911

Qy 242  AlaHisCysPheArgLysHisThrAspValPhe---------AsnTrpLysValArgAla  258
        ||||:::
Db 912  GCACACTGTGTT---------TATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTG   962

Qy 259  GlySerAspLysLeu---------GlySerPheProSerLeuAlaValAlaAlaLysIleIleIle 276
        |||
Db 963  GGTCTAGTTTCCCGTGTTGGACAATCCAGCCCCATCCCACCTGGTGGACAAGATTGTC--  1019

Qy 277  IleGluPheAsnProMetTyr---AspAsnAspIleAlaLeuMetLys             293
```

```
Db 697  :::.|||||||       :::.||||                    |||
        TCAAAAGCAGTGGTTCTTTACCCTGTATAGCCTGCGGGGTCAACTTGAACTCAAGCCGC   756

Qy 200  ThrProArgValValGlyGlyGluGluValAlaSerValAspSerTrpProTrpGlnValSer 219
Db 757  CAGAGCAGGATCGTGGGCGGCGAGAGCGCGTCCCCGGGGCCGCTCCCGGGCCCTGGCCAGGTCAGC 816

Qy 220  IleGlnTyrAspLysGlnHisValCysGlyGlyGlySerIleLeuAspProHisTrpValLeu 239
        :::                      ||||||
Db 817  CTGCACGTCCAGAACGTCCACGTGCGCGGAGGGTCCATCATCACCCCGAGTGGATCGTG    876

Qy 240  ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla  258
        ||||||||||||        :::  ::::::||||||
Db 877  ACAGCGCGCCCACTGCGTGGGAAAAACCTCTTAACATCATCCATTGGACGGCCATTGCG   936

Qy 259  GlySerAspLysLeuGlySerPhe---------ProSerLeuAlaValAlaLysIle    274
        |||               :::
Db 937  GGGATTTTGAGA---CAATCTTTCATGTTCTATGGAGCCGGATACCAAGTAGAAAAAGTG  993

Qy 275  IleIleIleGluPheAsnProMetTyr---------ProLysAspAsnAspIleAlaLeu  291
        |||
Db 994  ATT-------TCTCATCCAAATTATGACTCCAAGAACAATGACATTGCGCTG         1044

Qy 292  MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe  311
        ||||||||||||     ||:::|||||||||||
Db 1045 ATGAAGCTGCAGAAGCCTCTGACTTTCAACGACCCAGTGTGTCTGCCCAAC          1104

Qy 312  PheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLys  331
        ||||||                      ::|:||||||||
Db 1105 CCAGGCATGATGCTCGCGCCAGAACAGCTGCTGGATTTCCGGGTGGGGGGCCACCGAG    1164

Qy 332  GlnAsnGlyLysLysMetSerAspIleLeuLeuGlnAlaSerValGlnIleLeuAspSer  351
        :::             :::|||||||||:::::
Db 1165 GAGAAA--GGGAAGACCTCAGAAGTGCTGAACGCTGCCCAAGGTGCTTCTCATTGAGACA  1221

Qy 352  ThrArgCysAsnAlaAspAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAla  371
                ::: |||||||
Db 1222 CAGAGATGCACACAGCAGATATGTCTATGACAACCTGATCACCACAGGTTGTGCC       1281

Qy 372  GlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr  391
        ||||||||||||:::|||||||||||||||||
Db 1282 GGCTTCCTGCAGGGGGACACTGTCGGTTCTGCCAGGTGACCTGGAGGGCCTTCTGGTCACT 1341

Qy 392  GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly  410
        :::            :::|||||||||
Db 1342 TCGAAGACAATATCTGGTGGCGTGATAGGGGATCAAGCTGGGGTTCTGGCTGTGCCAAA   1401

Qy 411  ProSerThrProGlyValTyrThrLysValSerAlaTyrIleLeuAsnTrpIleTyrAsnVal 430
        :::              ||||||||||||||
Db 1402 GCTTACAGACCAGGAGTGTACGGGAATGTGATGGTATTCACGGACTGGATTTATCGACAA   1461

Qy 431  TrpLysAlaGlu                                                  434
        |||
Db 1462 ATGAGGGCAGAC                                                 1473
```

```
Qy   42 AlaSerIleIleIleValValValLeuIleLeuLysValLeuLeuAsp---------LysTyr  58
                                                        ::: :::::|||
Db  324 -----ATATTAGCACTGGCCATTGTCGTGGCATCCACTTCGACTGCTCAGGGAGTAC        377

Qy   59 -------TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu          74
                                                         :::  :::
Db  378 AGATGTCGCTCATCCTTTAAGTGT--------ATCGAGCTGATAACTCGA-------        419

Qy   75 CysAspGlyGluLeuAspCysProLeuGlyLysGluHisCysValLysSerPhe          94
         |||||||     ||||||||||        |||||||           :::::
Db  420 TGTGACGGAGTCTCGATTGCAAAGACGGGAGGAGACGAGTACCCGCTGT-----          467

Qy   95 ProGluGlyProAlaValAlaValAlaArgLeuSerLysAspArgSerThrLeuGlnValLeu  114
                                                                  ::: :::
Db  468 ------GTCCGGTGGGTGGGTCCAGAATGCCGTGCTCCAGGTGTTC                  506

Qy  115 AspSerAlaThrGlyAsnTrpPheSerAlaCysThrGlnAspAsnPheThrGluAlaLeuAla  134
         :::|||||   ||||:::              ||||||
Db  507 ACAGCTGCT-----TCGTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCA     560

Qy  135 GluThrAlaCysSerArgGlnMetGlyTyrSerSer----------------           145
Db  561 AATGTTGCCTGCTCCCAACTGGGTTTCCCAAGCTATGTAAGTTCAGATAACCTCAGAGTG    620

Qy  146 ----------LysProThrPheArgAlaValAlaGluIleGlyProAspGlnAspProLeuAspVal  162
Db  621 AGTCGCTGCTGAGGGGCAGTTCCGGAGCAGGAGTTGTGTCCATGACTCACCTCTTGCCAGAT    680

Qy  163 ValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCysLeu        182
Db  681 GACAAGGTGACTGCATTACACCACCTCAGTATATATGTGAGGGAGGGA-----TGTGCC      731

Qy  183 SerGlySerLeuValSerLeuHisCysSerLeuAlaCysGly---LysSerLeuLysThrPro  201
Db  732 TCTGCCCACGTGGTTACCTTGCAGTGCACAGCCTGTGGTCATAGAGGGGCTACAGTCA      791

Qy  202 ArgValValGlyGlyGluAlaAlaSerValAspSerTrpProTrpGlnValSerIleGln     221
         |||:::|||||::::
Db  792 CGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCTGCAGGCCAGCCTTCAG      851

Qy  222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla     241
         :::   |||:::               :::
Db  852 TTCCAGGGGTACCACCTGTGGGGGGCTCGTCATCAGCCCCGTGGATCATCACTGCT        911

Qy  242 AlaHis------------                                              243
         |||:::
Db  912 GCACCACTGTGTTATGAGATTGTAGCTCCTAGAGAAAGGGCAGACAGAAGAGGAAGAAG     971

Qy  244 ------CysPheArgLysHisThrAspValPhe-------                        252
         :::
Db  972 CTCCTGCTGTGCTGGAGGAAACCCACCAACAAAAATGAA-AGGACCTAGACCTTCCCATAGCTAATT 1030

Qy  253 -----------------------AsnTrpLysValArg                         257
                                 :::::
Db 1031 CCAGTGGACCATGTTATGGCAGATACAGGCTTGTACCTCCCAGTCATGGACCATCCAG    1090

Qy  258 AlaGlySerAspLysLeu------GlySerPheProSerLeuAlaValAlaLysIleIle     275
         |||                    :::
Db 1091 GTGGGCTCAGTTCCCTGTTGTGACAATCCAGCCCCATCCACTTCGTGGAGAAGATTGTC    1150
```

```
Db 1020 -----TACCAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAG    1073
         ||||||||||||||||||||||||||||||||||
Qy  294 LeuGlnPheProLeuThrPheSerGlyThrValArgProLeuCysLeuProPhePhe       313
         :::||::::||||||||:::
Db 1074 CTGGCCGGGCCACCACTCAGTTCAATGAAAATCCAGCCTGTGCCCCAACTCTGAA        1133

Qy  314 GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn    333
         |||||||:::|||||||||||
Db 1134 GAGAACTTCCCCGATGAAAAGTGTGCTGGACGTGCAGGATGGGGGGCCACA--GAGGAT    1190

Qy  334 GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleIleAspSerThrArg 353
         |||:::||||||:::
Db 1191 GGAGGGTGACGGCCTCCCCTGTCCTGAACCACGCGGCCGCGTCCCTTGATTTCCAACAAGATC 1250

Qy  354 CysAsnAlaAspAspAlaTyrGlnGlyGlnValThrGluLysMetCysAlaGlyTyrIle    373
         ||||||:::
Db 1251 TGCAACCACCAGGGACGTGTACGGTGGCATCATCTCCCCCTCTGCCGCGGGCTAC        1310

Qy  374 ProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSer    393
         :::||||||
Db 1311 CTGACCGGTGGGTGAACAGCTGCAGCGGGGGACAGCGGGGGCCCCCGGTGTGTCAAGAG    1370

Qy  394 AspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSer    412
         |||:::
Db 1371 AGGAGGCTGTGAAGTTAGTGGGAGCGACCCAGCTTTGGCATCGGCTGCGCAGAGGTGAAC   1430

Qy  413 ThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrpLys    432
         |||||||:::|||:::
Db 1431 AAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCGTGACTGGATCCACGAGCAGATGGAG   1490

Qy  433 AlaGluLeu                                                      435
         :::|||
Db 1491 AGAGACCTA                                                      1499
```

RESULT 8
US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

Alignment Scores:
Pred. No.:   Length: 2544
Score: 5.75e-58   Matches: 160
Percent Similarity: 627.00   Conservative: 73
Best Local Similarity: 48.14%   Mismatches: 150
Query Match: 33.06%   Indels: 102
DB: 26.77%   Gaps: 18
                    3

US-09-607-745-2 (1-435) x US-09-518-046-3 (1-2544)

```
Qy   22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleIleAlaLeuSerLeu    41
         :::|||                   |||:::||||||||||||||||||||
Db  273 CTGCCATTTGAGACTTTTTCCCAATCATCGTCATTGGGGATCATTGCATTG--------    323
```

```
Db   468  --------------------------------------GTCCGGTGGTGGTCAGAATGCCGTGCTCCAGTGTTC  506

Qy   115  AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaAlaLeuAla  134
               :::::|||
Db   507  ACAGCTGCT------TCGTGGAAGACCATGTGCTCCGATGACTGGAAGAGGGTCACTACGCA  560

Qy   135  GluThrAlaCysArgGlnMetGlyTyrSerSer---------------------------  145
Db   561  AATGTTGCCTGTGCCCAACTGGGTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTG  620

Qy   146  ---------LysProThrPheArgAlaValGluIleGlyProGlnAspLeuAspVal  162
               :::           |||
Db   621  AGTCGCTCGGAGGGCAGTTCCGGAGGAGTTGTGTCCATGATCACCTCTTGCCAGAT  680

Qy   163  ValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerGlyProCysLeu  182
               :::|||
Db   681  GACAAGGTGACTGCATTACCACCTCAGTATATGTGAGGGAGGGA-------TGTGCC  731

Qy   183  SerGlySerValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrPro  201
               |||:::
Db   732  TCTGGCCACGTGGTTACCTTGCCAGTGCACAGCCTGTGTCATAGAAGGGGCTACAGCTCA  791

Qy   202  ArgValValGlyGlyGluGluAlaLaSerValAspSerTrpProTrpProValSerIleGln  221
               ::: :::          |||:::||
Db   792  CGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCTGGCCAGGCCAGCCTTCAG  851

Qy   222  TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla  241
               :::     |||:::||
Db   852  TTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCACGCCCCGTGGATCATCATCACTGCT  911

Qy   242  AlaHisCysPheArgLysHisThrAspValPhe----------AsnTrpLysValArgAla  258
               |||||||          :::::
Db   912  GCACACTGTGTT--------------TATGACTTGACCTCCCAAGTCATGACCATCCAGGTG  962

Qy   259  GlySerAspLysLeu------------GlySerPheProSerLeuAlaValAlaLysIleIleIle  276
               ||| 
Db   963  GGTCTAGTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTT---  1019

Qy   277  IleGluPheAsnProMetTyr--ProLys-----AspAsnAspIleAlaLeuMetLys  293
               |||
Db   1020 ------TACCCAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAG  1073

Qy   294  LeuGlnPheProLeuThrPheSerGlyThrValArgProIleIleCysLeuProPhePheAsp  313
               |||||||:::
Db   1074 CTGGCCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTTCGAA  1133

Qy   314  GluGlyLeuThrProAlaTyrGlnGlyLeuPheThrLysGlnAsn  333
               |||
Db   1134 GGAAACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCCACA--GAGGAT  1190

Qy   334  GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg  353
               ||||||:::
Db   1191 GGAGGGTGACGCGTCCCCTGTCCTGAACCACGCGGGCCGTCCCTTTGATTCCACAAAGAT  1250

Qy   354  -CysAsnAlaAspAspAlaTyrGlnGlyLeuGluValThrGlyLysMetMetCysAlaGlyIl  373
               -:::           :::::
Db   1251 CTGCAACCACAGGGACGTGTACGGTGGCATCATCTCCCCTCGCGCGGGCTA  1310

Qy   373  eProGluGlyGlyValAspThr--CysGlnGlyAspSerGlyGlyProLeuMetTyrGln  392
               ||||||:::
Db   1311 CCTGACGGGTGGCGTTGGAACAGCTGCCAGGGGACAGCGCGGGGGGCCCCTGGTGTGTCAA  1370

Qy   393  SerAspGln--TrpHisValGlyIleValSerTrpGlyTyrGlyCysGlyGlyPro  411
               ::: |||
Db   1371 GAGAGGAGGCGTGGAAGTTAGTGGGCATGGCATCGGTGTGCGCAGACGTG  1430

Qy   412  SerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrp  431
               :::
Db   1431 AACAAGCCTGGGGTGTACACCCGTGTCACCCGTGCTTGGAACTGGATCCAGCAGCAGATG  1490

Qy   432  LysAlaGluLeu  435
               ::: |||
Db   1491 GAGAGAGACCTA  1502
```

```
Db   1319 GATCGGAGGTGACGGCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTCCAACAAG  1378

Qy   353  ArgCysAsnAlaAspAspAlaTyrGlnGlyLeuGluValThrGlyLysMetMetCysAlaGly  372
Db   1379 ATCTGCAACCACAGGGACGTGTACGGTGGCATCATCTCCCCTCGCGCGGGGC  1438

Qy   373  IleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln  392
               ||||||||:::
Db   1439 TACCTGACGGGTGGCGTTGGAACAGCTGCCAGGGGGACAGCGGGGGGGCCCCTGGTGTGTCAA  1498

Qy   393  SerAspGln---TrpHisValGlyIleValSerTrpGlyTyrGlyCysGlyGlyPro  411
               ::: :::
Db   1499 GAGAGGAGGCGTGTGGAAGTTAGTGGGACCAGCTTTGGCATCGGTGTGCGCAGAGGTG  1558

Qy   412  SerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrp  431
               ||||||||
Db   1559 AACAAGCCTGGGGTGTACACCCGTGTCACCCGTGCTTGGAACTGGATCCAGCAGCAGATG  1618

Qy   432  LysAlaGluLeu  435
               ::: |||
Db   1619 GAGAGAGACCTA  1630
```

RESULT 9
US-09-261-416-1

; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663e1 Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Alignment Scores:
Pred. No.:   Length: 2416
Score: 2.1e-57   Matches: 158
Percent Similarity: 621.50   Conservative: 72
Best Local Similarity: 51.57%   Mismatches: 150
Query Match: 35.43%   Indels: 66
DB: 26.54%   Gaps: 18
                    3

US-09-607-745-2 (1-435) x US-09-261-416-1 (1-2416)

```
Qy    22  IleProMetGluThrPheAspLysLysValGlyIleIleIleIleIleAlaLeuLeuSerLeu  41
               :::||| |||
Db   273  CTGCCATTGAAGTTTTTTCCCAATCATGTCCAATCATTGGGATCATTGCATTG--------  323

Qy    42  AlaSerIleIleIleValValLeuIleLeuLysValIleLeuAsp---------LysTyr  58
               :::   ::: :::
Db   324  ------ATATTAGCACTGGCCATTGGTCTGGGCATCCACTTGACCTGCTCAGGGAGTAC  377

Qy    59  ----------TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu  74
               ::: |||
Db   378  AGATGTCGCTCATCCTTAAGTGT--------ATCGAGCTGATAACTCGA---------  419

Qy    75  CysAspSerGlyLeuGluLeuAspCysProLeuGluAspGluGluHisCysValLysSerPhe  94
               |||||||||
Db   420  TGTGACGGAGTGCTCGGATTGGAAAGACGGGGAGGACGAGTACCGCTGT---------  467

Qy    95  ProGluGlyProAlaAlaAlaAlaArgGluSerLysAspArgSerThrLeuGlnValLeu  114
               ::: :::            |||||||||
```

```
RESULT 10
US-09-510-738A-188
; Sequence 188, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT:  O'Brien, Timothy J.
;   TITLE OF INVENTION:  Ovarian Cancer
;   TITLE OF INVENTION:  Compositions and Methods for the Early Diagnosis of
;   FILE REFERENCE:   D6223CIP-A
;   CURRENT APPLICATION NUMBER: US/09/510,738A
;   CURRENT FILING DATE:  2000-02-22
;   PRIOR APPLICATION NUMBER:   09/039,211
;   PRIOR FILING DATE:   03-14-1998
;   NUMBER OF SEQ ID NOS:  188
; SEQ ID NO 188
;   LENGTH: 1783
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: full length cDNA of hepsin
US-09-510-738A-188

Alignment Scores:
Pred. No.:      1.36e-53      Length:          1783
Score:          584.50        Matches:         140
Percent Similarity:   45.05%  Conservative:    60
Best Local Similarity:  31.53%  Mismatches:    161
Query Match:    24.96%        Indels:          83
DB:                           Gaps:            11
US-09-607-745-2 (1-435) x US-09-510-738A-188  (1-1783)
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Qy   19 LysProArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeu  38
            ::||||:::::::::::::::               |||||           :::::::::::
Db  288 AGACCCAAGGTGGCAGCTTCACT-------GCGGGACCCTGCTACTTTGACACGCC 338

Qy   39 LeuSerLeuAlaSerIleIleIleValValLeuIleLysValIleLeuAspLysTyr  58
            |||||   ||||||||||||:::::::
Db  339 ATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGG----------------- 380

Qy   59 TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysLeuGlnLeuCysAspGlyGlu  78
Db  380 ------------------------------------------------------------ 380

Qy   79 LeuAspCysProLeuGlyAspGluGluHisCysValLysSerPheProGluGlyPro  98
            :::|||||      |||:::::||:|||
Db  381 --------------------AGTGACCAGGAG------------------------CCG 395

Qy   99 AlaValAlaValAlaArgLeuLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
            ::||||||::::::|||            |||
Db  396 CTGTACCCAGGTGCAGCTCGTCGGACGCTCGGCTCAGCTCTTTGACAAGACGGAA 455

Qy  119 GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCys 138
            :::||||                       :::|||
Db  456 GGGACGTGGCGGCGTGCTGCTCCTCCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGC 515

Qy  139 ArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluValGlyIleGlyProAspGln 158
            ::||||                   |||:::
Db  516 GAGGAGATGGGCTTC-------------CTCAGGGCACTG-------ACCCACTCC 551

Qy  159 AspLeuAspValValGluIleGluThrGluAsn------------------------ 168
            ::||||||||||:|||
Db  552 GAGCTGGACGTGCGAACGGCGGGCGCCAATGCAGCTCGGGCTTCTCTGTGTGGACGAG 611

Qy  169 ------------SerGlnLeuArgMetArgAsnSerGlyProCysLeuSer 183
                        ::||||||||||||||||||||||||
Db  612 GGGGAGGCTGCCCCACACCCAGAGGCTGCTCGGAGGTCATCTCCGTGTGTGATTGCCCCAGA 671

Qy  184 GlySerLeuValSerLeuHisCysLeuAlaCysGly--LysSerLeuLysThrProArg 202
            ||||:::       :::||||      ||||       :::|||
Db  672 GGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGAAGCTGCCCGTGGACCGC 731
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Qy  203 ValValGlyGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGlnTyr 222
            ::::|||||||       ::|||
Db  732 ATCGTGGGAGGCCGGGACACCAGCTTGGCCCGTGGCCGTGGCCAAGTCAGCTTCGCTAT 791

Qy  223 AspLysGlnHisValCysGlyGlySerIleLeuAspGlySerTrpValLeuThrAlaAla 242
            ::||:::||||||||:::::|||
Db  792 GATGGAGCACACCTGTGGGGGATCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCC 851

Qy  243 HisCysPheArgLysHisThrAspValPheAsn---TrpLysValArgAlaGlySerAsp 261
            ||||||||                  :::       ||
Db  852 CACTGCTTCCCGGAGCGAACCGGGTCCTGTCCGATGCCGAGTGTTTGCCGGTGCCGTG 911

Qy  262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluProAsnPro 281
            |||              :::
Db  912 GCCCAGGCCTCTCCCCACGGGTCCAGCTGGGGGTGCAGCTGTGGTCTCCACCAGGGGGC 971

Qy  282 MetTyrPro-----------------LysAspAsnAspIleAlaLeuMetLys 293
                                       :::
Db  972 TATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCAC 1031

Qy  294 LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp 313
            |||                    |||
Db 1032 CTCTCCAGTCCCCTGCCCCTCCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGGC 1091

Qy  314 GluGluLeuThrProAlaThrProLeuTrpIleGlyTyrIleGlyTyrPheThrLysGlnAsn 333
            ::: :::             |||||
Db 1092 CAGGCCCTGGTGGATGGCAAGATCGTTACCGTGACAGGGTGGGGCAACACG--CAGTAC 1148

Qy  334 GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg 353
            |||||||                ::     :::|||
Db 1149 TATGGCCAACAGCCGGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTC 1208

Qy  354 CysAsnAlaAspAspAlaTyrGlnGlyGluValThrGluMetCysAlaGlyIle 373
            :::                ||||||
Db 1209 TGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTCTGGCTAC 1268

Qy  374 ProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln--- 392
            |||||||                 |||
Db 1269 CCCGAGAGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGAGGAC 1328

Qy  393 -------------SerAspGlnTrpHisValGlyIleValGlyIleSerTrpGlyTyrGlyCys 408
                         ::: :::     :::|||
Db 1329 AGCATCTCTGGACGCACCGGTTGGGGGCACTGGTGT 1388

Qy  409 GlyGlyProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyr 428
                                     |||:::       :::
Db 1389 GCCCTGGCCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTC 1448

Qy  429 AsnValTrpLys 432
            :::
Db 1449 CAGGCCATAAAG 1460
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RESULT 11
US-09-861-966-188
; Sequence 188, Application US/09861966
; Patent No. 6518028
; GENERAL INFORMATION:
; APPLICANT:  O'Brien, Timothy J.
;   TITLE OF INVENTION:  Compositions and Methods for the Early Diagnosis of
;   TITLE OF INVENTION:  Ovarian Cancer
;   FILE REFERENCE: D6223CIP-A/Div
;   CURRENT APPLICATION NUMBER:  US/09/861,966
;   CURRENT FILING DATE:  2001-05-21
;   PRIOR APPLICATION NUMBER: 09/510,738
;   PRIOR FILING DATE: 2000-02-22
;   NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188
;   LENGTH: 1783
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: full length cDNA of hepsin
US-09-861-966-188
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Db   1032   CTCTCCAGTCCCTGCCCTCACAGAATCATCCAGCGTGTGTGCTCCCAGTCGCCGGC   1091

Qy   314   GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn   333
       ::: ||||||| ::   :::
Db   1092   CAGGCCCTGGTGATGGCAAGATCGTACCGTGACGGGGCAACACG---CAGTAC   1148

Qy   334   GlyGlyLysMetSerAspIleIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg   353
       ::: .. :::   :::   ::   ::   ::|||
Db   1149   TATGGCCAACAGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTC   1208

Qy   354   CysAsnAlaAspAspAlaTyrArgGlnGlyGluValThrGluLysMetMetCysAlaGlyIle   373
       ||||| :::::
Db   1209   TGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTAC   1268

Qy   374   ProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln--   392
       |||||||| ::   :::
Db   1269   CCCGAGGGTGGCCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGAGGAC   1328

Qy   393   --------SerAspGlnTrpHisValValGlyIleValSerTrpGlyTyrGlyCys   408
       :::   :::
Db   1329   AGCATCTCTGGACGCCACGTTGGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGT   1388

Qy   409   GlyGlyProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyr   428
       ||||||||
Db   1389   GCCCTGGCCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTC   1448

Qy   429   AsnValTrpLys   432
       |||
Db   1449   CAGGCCATAAAG   1460

RESULT 12
US-09-742-703-3
; Sequence 3, Application US/09742703
; Patent No. 6423543
; GENERAL INFORMATION:
; APPLICANT: Patrick Allen Marcotte
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPSIN EXPRESSION
; FILE REFERENCE: RTS-0090
; CURRENT APPLICATION NUMBER: US/09/742,703
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (826)..(2079)
US-09-742-703-3

Alignment Scores:
Pred. No.:   2.11e-53   Length: 2363
Score: 584.50   Matches: 140
Percent Similarity: 45.05%   Conservative: 60
Best Local Similarity: 31.53%   Mismatches: 161
Query Match: 24.96%   Indels: 83
DB: Gaps: 11

US-09-607-745-2 (1-435) x US-09-742-703-3 (1-2363)

Qy   19   LysProArgIleProMetGluThrProArgLysValGlyIleProIleIleAlaLeu   38
      ::: |||||::   ::::|||||
Db   868   AGACCCAAGGTGCAGCTCTCACT-------GCGGGGACCCTGCTACTTCTGACAGCC   918

Qy   39   LeuSerLeuAlaSerIleIleIleValValLeuIleLysValIleIleLeuAspLysTyr   58
      :::
Db   919   ATCGGGGCGGCATCCTGGGCCATTGGCTGTTCTCCTCAGG--------   960

Qy   59   TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu   78
Db   960   --   960

Alignment Scores:
Pred. No.:   1.36e-53   Length: 1783
Score: 584.50   Matches: 140
Percent Similarity: 45.05%   Conservative: 60
Best Local Similarity: 31.53%   Mismatches: 161
Query Match: 24.96%   Indels: 83
DB: Gaps: 11

US-09-607-745-2 (1-435) x US-09-861-966-188 (1-1783)

Qy   19   LysProArgIleProMetGluThrProArgLysValGlyIleProIleIleAlaLeu   38
      ::: |||||::   :::::::::
Db   288   AGACCCAAGGTGCAGCTCTCACT-------GCGGGGACCCTGCTACTTCTGACAGCC   338

Qy   39   LeuSerLeuAlaSerIleIleIleValValLeuIleLysValIleIleLeuAspLysTyr   58
Db   339   ATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCCTCAGG---------   380

Qy   59   TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu   78
Db   380   --   380

Qy   79   LeuAspCysProLeuGlyGlyAspGluHisCysValLysSerPheGluGlyPro   98
      |||:||| :::|||
Db   381   ------------------AGTGACCAGAG---------CCG   395

Qy   99   AlaValAlaAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThr   118
      ||:::|||| ::: ||| |||
Db   396   CTGTACCCAGTGCAGTCAGCTCGCGACGCTCGGCTCATGGTCTTTGACAAGACGGAA   455

Qy   119   GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaGluThrAlaCys   138
      :::|||
Db   456   GGGACGGTGGCGGCTGCTGTGTCCTCCGGCTCCAACGCCAGGGTAGCCGGACTCAGCTGC   515

Qy   139   ArgGlnMetGlyTyrSerSerSerlysProThrPheArgAlaValGluIleGlyProAspGln   158
      :::||||| :::
Db   516   GAGGAGATGGGCTTC------------------CTCAGGGACTG-----ACCCACTCC   551

Qy   159   AspLeuAspValValGlyIleIleThrGluAsn-----   168
      ::|||||
Db   552   GAGCTGGACGTGCGAACGGGCGGCGGCCAATGCAGCTGCCTTCTTCTGTGTGGACGAG   611

Qy   169   --------SerGlnLeuLeuArgMetArgAsnSerSerGlyProCysLeuSer   183
      :::|||
Db   612   GGGAGGCTGCCCCACACCAGAGCTGCTGGAGGTCATCTCCGTGTGATTGCCCCAGA   671

Qy   184   GlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrProArg   202
      |||||||| ::: |||
Db   672   GGCCGTTCTTGGCCCGCATCTGCCAAAGACTGTGCCGCAGAAGTGCCCGTGGACGGC   731

Qy   203   ValValGlyGlyGluGluAlaSerValAspSerProTrpProTrpGlnValSerIleGlnTyr   222
      :::|||||| :: ||||
Db   732   ATCGTGGGAGGCGGGGACACCAGTGTTGGGCCGTGGCCAAGTCAGCCTTCGCTAT   791

Qy   223   AspLysGlnHisValCysGlyGlySerIleLeuAspHisProHisValLeuThrAlaAla   242
      |||||||| :::|||||
Db   792   GCCCAGGCCGCCTCCCCAGGTCTGCAGCCTGGGGGTGCAGCTGGTGCTACCACGGGGGC   851

Qy   243   HisCysPheArgLysHisThrAspValPheAsn---TrpLysValArgAlaGlySerAsp   261
      |||:: |||::   :::
Db   852   CACTGCTTCCGGGAGCACACCGGGGTCTTCAACTGGAAGGTCCGGGCCGGGTCGGTG   911

Qy   262   LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleGluGluAsnPro   281
      :::   :::
Db   912   GCCCAGGCCGCCTCCCCAGGTCTGCAGCCTGGGGGTGCAGCTGGTGCTACCACGGGGGC   971

Qy   282   MetTyrPro------------------LysAspAsnAspIleAlaLeuMetLys   293
      ::: |||||
Db   972   TATCTTCCCTTTCGGGACCCCAACAGCGGAGAGAACAGCAAGCGATATTGCCCTGGTCAC   1031

Qy   294   LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp   313
      :::::|||:|||||:||||||
Db   294   --

Db   1969 GCCCTGGCCCAGAAGCCAGGCGTCTACACCACCAAAGTCACTCAGTCAGTGACTTCCGGGAGTGGATCTTC 2028
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Qy   429 AsnValTrpLys 432
               |||
Db   2029 CAGGCCATAAAG 2040

RESULT 13
US-09-820-002-1
; Sequence 1, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
;   APPLICANT: Gan, Weiniu
;   APPLICANT: Ye, Jane
;   APPLICANT: DiFrancesco, Valentina
;   APPLICANT: Beasley, Ellen
;   TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: CL001194
;   CURRENT APPLICATION NUMBER: US/09/820,002
;   CURRENT FILING DATE: 2001-03-29
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1615
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-820-002-1

Alignment Scores:
Pred. No.:   Length: 1615
Score: 3.6e-53   Matches: 132
Percent Similarity: 580.00   Conservative: 57
Best Local Similarity: 44.06%   Mismatches: 146
Query Match: 30.77%   Indels: 94
                          24.77%   Gaps: 9

US-09-607-745-2 (1-435) x US-09-820-002-1 (1-1615)

Qy   19 LysProArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaAlaLeu 38
               ::::||:::::
Db   220 AGACCAAGGTGGCAGCTCTCACT------GCGGGGACCCTGCTACTTCTGACAGCC 270

Qy   39 LeuSerLeuAlaSerIleIleIleValValIleLeuGluLysValIleLeuLeuAspLysTyr 58
               ::: |||||||||||
Db   271 ATCGGGCGCCATCCTGGGCCATTGTGGCTATTGTGCGTGTTCTCCTCAGG------ 312

Qy   59 TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu 78
Db   312 -- 312

Qy   79 LeuAspCysProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyPro 98
               |||
Db   313 ------------------------------AGTGACCAGGAG- 327

Qy   99 AlaValAlaValArgSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
               ::: |||||||||
Db   328 CTGTACCAGTGCAGGCCAGGTCGCAGCTCCGGCAGCGCTCGGGCTCCATGGTCTTTGACAAGACGGAA 387

Qy   119 GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaLeuThrAlaCys 138
               ||||||| :::||||
Db   388 GGGACGTGGCGGCTGCTGTCTCCTCGGCTCCAAGCCCAGGGTAGCCGGACTCAGCTGC 447

Qy   139 ArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGln 158
               ::::||||||
Db   448 GAGGAGGATGGGCTTCCTCAGT------ 468

Qy   159 AspLeuAspValAlaValGluIleThrGluAsnSerGlnLeuLeuArgMetArgAsnSer 178
               ::::|||||
Db   468 -- 468

Qy   179 GlyGlyProSerThrProGlyValTyrThrLysValSerLeuAlaTyrLeuAsnTrpIleTyr 197

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/000,846
    FILING DATE: 30-DEC-1997
    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/866,058
    FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
    NAME: LEBOVITZ, RICHARD M.
    REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: BERLX 65P1
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 703-243-6333
    TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
    LENGTH: 1605 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
    ORGANISM: Mus musculus
FEATURE:
    NAME/KEY: CDS
    LOCATION: 35..1282
US-09-000-846-1
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Alignment Scores:
Pred. No.:                                Length:           1605
Score:                  5.88e-53          Matches:           136
Percent Similarity:     578.00            Conservative:       58
Best Local Similarity:  47.43%            Mismatches:        152
Query Match:            33.25%            Indels:             63
DB:                     24.68%            Gaps:               11
                        2
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US-09-607-745-2 (1-435) x US-09-000-846-1 (1-1605)

Qy    62  CysGlyGlnProLeuHisPheIleProArgLysGln------LeuCysAspGlyGluLeu  79
                                              ::  :
Db    97  TGTGGGTACCCTGCT-----GTTCTGACAGGCATTGGGGCCGCGTCCTGGGCCATTGT  150

Qy    80  AspCysProLeuGlyGlu-AspGluGluHisCysValLysSerPheProGluGlyProAl  99
               ::   :::   :::::  ::                  :::::
Db   244  AACGTGGAGGCTACTGGCGTCTCCTCACGCTCCAATGCCAGGGTGGCAGGGCCTCGGCTGTGA  303

Qy   100  ------------------------------------------------------------CCACT  183
Db   151  GACCATCCTACTGCAGAGTGACCAGGAG-------------------------------CCACT  183

Qy    99  aValAlaValArgLeuSerLysAspAspArgSerThrLeuGlnValLeuAspSerAlaThrGl  119
              :::::     :::                  ::     ::      :::
Db   184  GTACCAAGTGCAGCTCAGTCCAGGGACTCACGGCTTGCGGTGTTTGACAAGACGGAGGG  243

Qy   119  yAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaGluThrAlaCysAr  139
              ::  :                       :::::
Db   244  AACGTGGAGGCTACTGGCGTCTCCTCACGCTCCAATGCCAGGGTGGCAGGGCCTCGGCTGTGA  303

Qy   139  gGlnMetGlyTyr-----------------------------------------------  143
              ::::::
Db   304  GGAGATGGGCTTCTCAGGGCTCTGGCGACTCGGAGCTGGATGTCCGCACTCGGGGCGC  363

Qy   144  -SerLysProThrPheArgAlaValGluIleGly------------------ProAspGlnAs  159
                                                           :::
Db   364  CAACGGCACATCGGGCTTCTTTTGCGTGGACGAGGCGGACTCCGTCTGGCTCGGAGGTT  423

Qy   159  pLeuAspValValGluIleThrGluAsnSerGlnLeuArgMetArgAsnSerSerGl  179
              ::::::      :::   :::      ::::
Db   424  GCTGGATGTGCATCCTCTGTATGTGAC---------------------------  448

Qy   179  yProCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGly--LysSerLe  198
```

```
Db   469  ---GAATTGCCCCAGAGGCCGTTCTTGGCCCCATCTGCCCAAGACGTGCCGCCAGGAAG  525
                ||||||                   :::::      ||||||
Qy   198  LeuLysThrProArgValAlaGlyGlyGluGlnLysSerValAspSerValAspSerTrpProTrpGln  217

Qy   526  CTGCCCGTGGACCGCATCGGAGGAGGCCGGACACCAGCTTGGGCCGGTGGCCGTGGCAA  585

Qy   218  ValSerIleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrp  237
              ||||||:::||||||                ::||||||||:::||||||
Db   586  GTCAGCCTTCGCTATGATGACAAGCACACCTCGTGGGGGGATCCCTGCTCTCCGGGGACTGG  645

Qy   238  ValLeuThrAlaAlaHisCysPheAspAsnPheThrGluAspSerValPheGlnAsn---TrpLysVal  256
              ||||||      :::      ||||||      :::      ||||||:::||||||
Db   646  GTGCTGACAGCCGCCCACTGCTTCGACAATTTCCCGGAGGCGAACCGGATCCCCGATGCCGAGTG  705

Qy   257  ArgAlaGlySerAspLysLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIle  276
              ||||||                         :::
Db   706  TTTGCCGGTGCCGTGGCCGGAGGGTGCAGCCTCTCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTG  765

Qy   277  IleGluPheAsnProMetTyrPro----------------LysAspAsnAsp  288
                  :::
Db   766  GTCTACCACGGGGGGCTATCTTCCCTTTCGGACCCCACACAGCGAGGAGAAACAGCAACGAT  825

Qy   289  IleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCys  308
              ||||||:::||||||      :::||||||:::||||||:::|||||||||||||||
Db   826  ATTGCCCTGGTCCAGTCCACTCTCCAGTCCCTGCCCTCACAGAATACATCCAGCCTGTGTGC  885

Qy   309  LeuProPhePheAspGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGly  328
                  :::                    ||||||
Db   886  CTCCCAGCTGCGCGCCGGGCCGCGGGCCCTGGTGATGGCAAGATCTGTACCGTGACGGGCTGGGGGC  945

Qy   329  PheThrLysGlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnVal  348
              ||||||      :::                        :::      :::
Db   946  AACACG--CAGTACTATGGCCAACAGCCCGGGGTACTTCCAGGAGGCTCCAGTCCCCATA  1002

Qy   349  IleAspSerThrArgCysAsnAlaAlaAspAspAlaTyrGlnGlyGluValThrGluLysMet  368
              ||||||      :::                  ||||||      :::
Db  1003  ATCAGCAATGAGTGTCTGCAATGGCGGCTGACTTCTCATGGAAACCAGATCAAGCCCAAGATG  1062

Qy   369  MetCysAlaGlyIleProGluGlyGlyValAspAspThrCysGlnGlyAspSerGlyGlyPro  388
              ||||||:::      :::      ||||||||||||:::||||||
Db  1063  TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCGTACGGCCGACACGGGTGGTCCC  1122

Qy   389  LeuMetTyrGln-----------SerAspGlnTrpHisValAlaValGlyIleValSer  403
              ||||||:::      :::      :::
Db  1123  TTTGTGTGTGAGGCAGCAGCATCTCCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT  1182

Qy   404  TrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrArgLysValSerAlaTyr  423
              :::||||||            ||||||      :::
Db  1183  TGGGGCACTGGCTGTGGCCTGTGCCCTGGCCCAGAAGCCAGGCGGTCTACACCAAGGTCAGTGACTTC  1242

Qy   424  LeuAsnTrpIleTyrAsnValTrpLys  432
              ||||||||||||:::||||||
Db  1243  CGGGAGTGGATCTTCTCCAGGCCATAAAG  1269
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RESULT 14
US-09-000-846-1
; Sequence 1, Application US/09000846
; Patent No. 5981830
; GENERAL INFORMATION:
;  APPLICANT: WU, QINGYU
;  APPLICANT: SADLER, JASPER
;  TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH
;  TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
;  NUMBER OF SEQUENCES: 8
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;   STREET: 2200 CLARENDON BLVD. SUITE 1400
;   CITY: ARLINGTON
;   STATE: VA
;   COUNTRY: US
;   ZIP: 22201
;  COMPUTER READABLE FORM:
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; SEQ ID NO 80
;   LENGTH: 1460
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-370-838-80

Alignment Scores:
Pred. No.:                  8.37e-53        Length:           1460
Score:                      576.00          Matches:           145
Percent Similarity:         50.88%          Conservative:       86
Best Local Similarity:      31.94%          Mismatches:        161
Query Match:                24.59%          Indels:             62
Db:                                  4      Gaps:               16

US-09-607-745-2 (1-435) x US-09-370-838-80 (1-1460)

Qy      5 SerAspGlnProLeuAsnSerLeuAlaLysProLeuAspLysProLeuArgIleProMet     24
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Db     19 GCAGAAAAAGAACCTCTTCATTAAGGATTAAAATGTTAGGCGACCACGTA--ACT        75

Qy     25 GluThrPheArgLysValGlyIleProIleIleIleIleAlaLeuLeuSerLeuAlaSerIle     44
            |||            :::          ::: |||
Db     76 TCGACTTCAAGATTTCTGAAT--CCATATGAGTATGTTCATTGTCGTCGCAGGGGTA      132

Qy     45 IleIleValValValLeuIleLeuLysValIleIleLeuAspLysTyrTyrPheLeuCysGlyGln     64
            :::|:|:::|                    ::::::|
Db    133 GTGATCCTGGCAGTCACCATAGCTCTACTTGTT----TACTTTTTAGCTTTTGAT       183

Qy     65 ProLeuHisPheIleProArgLys------GlnLeuCysAspGlyLeuGluAspCysPro     82
            :::                                  :::|
Db    184 CAAAAATCTTACTTTTATAGGAGCAGTTTCAACTCCTAAATGTTGAATATAATAGTCAG     243

Qy     83 Leu-----                                      GlyGluAspGluGlnHisCys     90
            :::                                          |||
Db    244 TTAAATTCACCAGCTACACAGGAATACAGGACTTTGAGTGGAAGAATTGGAATCTCTGATT      303

Qy     91 ValLysSerPheProGluGly----                        ProAlaValAlaValArg     103
            ||||                                           :::
Db    304 ACTAAAACATTCAAAGAATCAAAATTTAAGAAATCAGTTCATCAGAGCTCATGTTGCCAAA     363

Qy    104 LeuSerLysAsp------                    ArgSerThrLeuGlnValLeuAspSerAlaThrGly     119
            ||||:                                :::  :::
Db    364 CTGAGGCAAGATGGTGTAGTGCGGATGTGTTGTCATGAAAATTTCAATTCACTAGA       423

Qy    120 AsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArg     139
            :::  :::                                        :::
Db    424 AATAACAGAAGCGAGCATCAATG-------------AAAAGCAGAATTGAGTCTGTTTTACGA     471

Qy    140 GlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAsp     159
            :::                                    :::|||
Db    472 CAAATGCTGAATAACTCT-----------GGAAACCTGGAAATAAACCCT-----TCA     513

Qy    160 LeuAspValValGlyIleThrGluAsnSerGlnGluLeuArgMetArgAsn------Ser     177
            :::      ::::::          :::
Db    514 ACTGAGGATAACATCACTTACTGACCAGGCTGCAGCAAATTGGCTTATTAATGAATGTGGG     573

Qy    178 SerGlyProCysLysSerGlyLeuSerLeuValSerLeuHisCysSerLeuAlaCysGlyLysSer     197
            :::|||||
Db    574 GCCGGTCCAGACCTAATA----------------------------------ACA     594

Qy    198 LeuLysThrProArgValValGlyGluGluAlaSerValAspSerTrpProTrpGln     217
            |||            ||||||
Db    595 TTGTCTGAGCAGGAAATCCTTGGACGCACTGAGGCTGGAGGAAGCTGGCCGTGGCAA     654

Qy    218 ValSerIleGlnTyrAspLysProLysValCysGlyGlySerIleLeuAspProHisTrp     237
            |||                                  ::::::
Db    655 GTCAGTCTGCGGCTCAATAATGCCCACCACTGTGGAGGCAGCCTGATCAATAACATGTGG     714

Qy    238 ValLeuThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArg     257
            ::::::|||                                    :::|
Db    715 ATCCTGACACAGCTCACTCGTCTTCAGAAGCAACTCTAATCCTCGTGACTGGATTGCCACG     774

Qy    258 AlaGlySerAspLeuLeuGlySerPheProSerLeu-----AlaValAlaLysIleIle     275
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Db       :::.|||                                        :::.||||||    |||                    |||.::
     775 TCTGGTATTCCACA------ACATTCCTAAACTAAGAATGAGAGTAAGAAATATTTA  828

Qy   276 IleIleGluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGln  295
                                  ||| ::|||||||||||||||||||||||||||::.:::
Db   829 ATTCATAACAATTATAAATCGCAACTCATGAAAATGACATTGCACTTGTGAGACTTGAG  888

Qy   296 PheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGlu  315
             :::.|||||||:::     :::.|||||||||                   :::
Db   889 AACAGTGTCACCTTTACCAAAGATATCCATAGTGTGTTCTCCCAGCTGCTACCCAGAAT  948

Qy   316 LeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGly  335
             :::.|||   .::::::  ||||||||   |||     :::       |||
Db   949 ATTCCACCTGGCTCTACTGCTTATGTAACAGGATGGGGCGCTCAAGAATATGCTGGCCAC 1008

Qy   336 LysMetSerAspIleLeuLeuGlnAlaSerValGlnAsnValIleAspSerThrArgCysAsn  355
             ||                :::     |||||||||||||::::||||||||||||||||||
Db  1009 ACAGTTCCAGAG--CTAAGCAAGGACAGGTCAGAATAATAAGTAATGATGTATGTAAT 1065

Qy   356 AlaAspAspAlaTyrGlnGlyGlyValThrGluLysMetCysAlaGlyTyrIleProGlu  375
             |||        ||| ::     ::. |||||||||||||||||||:::||||::::
Db  1066 GCACCACATAGTTATAATGGAGCCATCTTGTCTGGAATGCTGTGTCTGGAGTACCTCAA 1125

Qy   376 GlyGlyValAspThrCysGlnGlyGlyTyrGlyLeuMetTyrGlnSerAspGln  395
             ||||||||||||||||||||||||||||||:::           :::
Db  1126 GGTGGAGTGGACGCATGTCAGGGTGACTCTGGTGGCCCACTAGTACAAGAAGACTCACGG 1185

Qy   396 ------TrpHisValValGlyValIleValSerTrpGlyTyrGlyCysGlyGlyProSerThr  413
             |||  :::.||||||||||||||||||||||:::.:|||||   |||
Db  1186 CGGCTTTGGTTTATTGTGGGGATAGTAAGCTGGGGAGATCAGTGTGGCCTGCCGGATAAG 1245

Qy   414 ProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIle  427
             ||||||||||||||||||||||:::.:|||||||||
Db  1246 CCAGGAGTGTATACTCGAGTGACACAGCCTACCTGACTGATT 1287
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Search completed: December 2, 2003, 02:54:14
Job time : 107.769 secs

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                GenCore version 5.1.6
      Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   December 2, 2003, 02:15:49 ; Search time 324.904 Seconds
                                       (without alignments)
                                       246.943 Million cell updates/sec

Title:          US-09-607-745-2
Perfect score:  2342
Sequence:       1 MDPDSDQPLNSLDVKPLRKP.......VYTKVSAYLNWIYNVWKAEL 435

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters:    673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA:*
         1:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
         2:  /cgn2_6/ptodata/2/pubpaa/pubpaa.PCT_NEW_PUB.pep:*
         3:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
         4:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
         5:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
         6:  /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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         8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
         9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
        10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
        11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
        12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
        13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
        14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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        16:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
        17:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
        18:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2338	99.8	435	12	US-10-180-719-6	Sequence 6, Appli
2	2337	99.8	437	9	US-09-851-588-8	Sequence 8, Appli
3	2319	99.0	437	11	US-09-776-191-4	Sequence 4, Appli
4	2297.5	98.1	432	11	US-09-888-257A-7	Sequence 7, Appli
5	2297.5	98.1	432	11	US-09-946-374-275	Sequence 275, App
6	2297.5	98.1	432	12	US-10-015-387A-275	Sequence 275, App
7	2297.5	98.1	432	12	US-10-063-735-112	Sequence 112, App
8	2297.5	98.1	432	12	US-10-006-130A-275	Sequence 275, App
9	2297.5	98.1	432	12	US-10-199-672-330	Sequence 330, App
10	2297.5	98.1	432	12	US-10-006-172A-275	Sequence 275, App
11	2297.5	98.1	432	12	US-10-187-749-330	Sequence 330, App
12	2297.5	98.1	432	12	US-10-194-457-330	Sequence 330, App
13	2297.5	98.1	432	12	US-10-184-642-330	Sequence 330, App
14	2297.5	98.1	432	12	US-10-196-747-330	Sequence 330, App
15	2297.5	98.1	432	12	US-10-015-392A-275	Sequence 275, App
16	2297.5	98.1	432	12	US-10-017-253A-275	Sequence 275, App
17	2297.5	98.1	432	12	US-10-173-689-330	Sequence 330, App
18	2297.5	98.1	432	12	US-10-173-690-330	Sequence 330, App
19	2297.5	98.1	432	12	US-10-173-691-330	Sequence 330, App
20	2297.5	98.1	432	12	US-10-173-692-330	Sequence 330, App
21	2297.5	98.1	432	12	US-10-173-694-330	Sequence 330, App
22	2297.5	98.1	432	12	US-10-173-698-330	Sequence 330, App
23	2297.5	98.1	432	12	US-10-173-699-330	Sequence 330, App
24	2297.5	98.1	432	12	US-10-173-707-330	Sequence 330, App
25	2297.5	98.1	432	12	US-10-174-569-330	Sequence 330, App
26	2297.5	98.1	432	12	US-10-174-583-330	Sequence 330, App
27	2297.5	98.1	432	12	US-10-174-587-330	Sequence 330, App
28	2297.5	98.1	432	12	US-10-174-589-330	Sequence 330, App
29	2297.5	98.1	432	12	US-10-174-591-330	Sequence 330, App
30	2297.5	98.1	432	12	US-10-175-736-330	Sequence 330, App
31	2297.5	98.1	432	12	US-10-175-742-330	Sequence 330, App
32	2297.5	98.1	432	12	US-10-175-744-330	Sequence 330, App
33	2297.5	98.1	432	12	US-10-175-745-330	Sequence 330, App
34	2297.5	98.1	432	12	US-10-175-748-330	Sequence 330, App
35	2297.5	98.1	432	12	US-10-175-751-330	Sequence 330, App
36	2297.5	98.1	432	12	US-10-175-754-330	Sequence 330, App
37	2297.5	98.1	432	12	US-10-176-480-330	Sequence 330, App
38	2297.5	98.1	432	12	US-10-176-489-330	Sequence 330, App
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40	2297.5	98.1	432	12	US-10-176-755-330	Sequence 330, App
41	2297.5	98.1	432	12	US-10-176-759-330	Sequence 330, App
42	2297.5	98.1	432	12	US-10-176-920-330	Sequence 330, App
43	2297.5	98.1	432	12	US-10-176-922-330	Sequence 330, App
44	2297.5	98.1	432	12	US-10-176-924-330	Sequence 330, App
45	2297.5	98.1	432	12	US-10-176-984-330	Sequence 330, App

ALIGNMENTS

```
RESULT 1
US-10-180-719-6
; Sequence 6, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;             Hillman, Jennifer L.
;             Yue, Henry
;             Guegler, Karl J.
;             Corley, Neil C.
;             Tang, Tom Y.
;             Shah, Purvi
;  TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
;  NUMBER OF SEQUENCES: 24
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Dr.
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/180,719
;     FILING DATE: 25-Jun-2002
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/008,271
;     FILING DATE: 16-Jan-1998
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Mohan-Peterson, Sheela
;     REGISTRATION NUMBER: 41,201
;     REFERENCE/DOCKET NUMBER: PF-0458 US
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-855-0555
```

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;       TELEFAX: 650-845-4166
;  INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 435 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: COLNNOT13
;       CLONE: 1337018
;  SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

US-10-180-719-6

Query Match             99.8%;  Score 2338;  DB 12;  Length 435;
Best Local Similarity   99.8%;  Pred. No. 5.3e-226;
Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVLIKVLLDKYYF 60
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Db    1 MDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVLIKVLLDKYYF 60

Qy   61 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN 120
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Db   61 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN 120

Qy  121 WFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGP 180
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Db  121 WFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGP 180

Qy  181 CLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT 240
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Db  181 CLSGSLVSLHCLACGESLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT 240

Qy  241 AAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEEFNPMYPKDNDIALMKLQFPLTF 300
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Db  241 AAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEEFNPMYPKDNDIALMKLQFPLTF 300

Qy  301 SGTVRPICLPFFDEELTPATPLMWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY 360
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Db  301 SGTVRPICLPFFDEELTPATPLMWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY 360

Qy  361 QGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKV 420
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Db  361 QGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKV 420

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Db  421 SAYLNWIYNVWKAEL 435


RESULT 2
US-09-851-588-8
; Sequence 8, Application US/09851588
; Patent No. US20020042067A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David
;  APPLICANT: Gish, Kurt C.
;  APPLICANT: Wilson, Keith E.
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
;  TITLE OF INVENTION: METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS
;  FILE REFERENCE: A-68829-1/DJB/JJD/AMS
;  CURRENT APPLICATION NUMBER: US/09/851,588
;  CURRENT FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/642,252
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: US 09/656,002
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;  LENGTH: 437
;  TYPE: PRT
;  ORGANISM: Homo sapiens
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US-09-851-588-8

Query Match             99.8%;  Score 2337;  DB 9;  Length 437;
Best Local Similarity  100.0%;  Pred. No. 6.7e-226;
Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVLIKVLLDKYYFL 61
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Db    4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVLIKVLLDKYYFL 63

Qy   62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy  122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
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Db  124 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 183

Qy  182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
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Db  184 LSGSLVSLHCLACGESLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 243

Qy  242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEEFNPMYPKDNDIALMKLQFPLTFS 301
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Db  244 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEEFNPMYPKDNDIALMKLQFPLTFS 303

Qy  302 GTVRPICLPFFDEELTPATPLMIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 361
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Qy  422 AYLNWIYNVWKAEL 435
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Db  424 AYLNWIYNVWKAEL 437


RESULT 3
US-09-776-191-4
; Sequence 4, Application US/09776191
; Publication No. US2003011916BA1
; GENERAL INFORMATION:
;  APPLICANT: Edwin L. Madison
;  APPLICANT: Edgar O. Ong
;  APPLICANT: Jiunn-Chern Yeh
;  APPLICANT: Corvas International, Inc.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING    THE ENCODED PROTEINS AND
;  TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES,
;  TITLE OF INVENTION: METHODS BASED THEREON
;  FILE REFERENCE: 24745-1607
;  CURRENT APPLICATION NUMBER: US/09/776,191
;  CURRENT FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/213,124
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/234,840
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/179,982
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: 60/183,542
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: 09/657,968
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;  LENGTH: 437
;  TYPE: PRT
;  ORGANISM: Homo Sapien
US-09-776-191-4

Query Match             99.0%;  Score 2319;  DB 11;  Length 437;
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Best Local Similarity  99.5%;  Pred. No. 4.3e-224;
Matches    432;  Conservative   0;  Mismatches   2;   Indels   0;   Gaps   0;

Qy    2  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL   61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL   63

Qy   62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  121
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  123

Qy  122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC  181
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC  183

Qy  182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  243

Qy  242  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS   301
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS   303

Qy  302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  304  GTVRLICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  363

Qy  362  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  364  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  423

Qy  422  AYLNWIYNVWKAEL  435
         |||||||||||||
Db  424  AYLNWIYNVWKAEL  437
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RESULT 4
US-09-888-257A-7
; Sequence 7, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER:.PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
;
; SEQ ID NO 7
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-888-257A-7

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Query Match          98.1%;  Score 2297.5;  DB 11;   Length 432;
Best Local Similarity 98.8%;  Pred. No. 6.1e-222;
Matches    429;  Conservative   0;  Mismatches   0;   Indels   5;   Gaps   1;

Qy    2  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL   61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL   63

Qy   62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  121
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  123

Qy  122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC  181
         |||||||||||||||||||||||           |||||||||||||||||||||||||
Db  124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC  178

Qy  182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  241
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  238

Qy  242  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS   301
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS   298

Qy  302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  358

Qy  362  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  418

Qy  422  AYLNWIYNVWKAEL  435
         |||||||||||||
Db  419  AYLNWIYNVWKAEL  432
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RESULT 5
US-09-946-374-275
; Sequence 275, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716   PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-01   PRIOR APPLICATION NUMBER: 60/100711
PRIOR APPLICATION NUMBER: 60/098723   PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-01   PRIOR APPLICATION NUMBER: 60/100848
PRIOR APPLICATION NUMBER: 60/098749   PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-01   PRIOR APPLICATION NUMBER: 60/100849
PRIOR APPLICATION NUMBER: 60/098750   PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-01   PRIOR APPLICATION NUMBER: 60/100919
PRIOR APPLICATION NUMBER: 60/098803   PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-02   PRIOR APPLICATION NUMBER: 60/100930
PRIOR APPLICATION NUMBER: 60/098821   PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-02   PRIOR APPLICATION NUMBER: 60/101014
PRIOR APPLICATION NUMBER: 60/098843   PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-02   PRIOR APPLICATION NUMBER: 60/101068
PRIOR APPLICATION NUMBER: 60/099536   PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101071
PRIOR APPLICATION NUMBER: 60/099596   PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101279
PRIOR APPLICATION NUMBER: 60/099598   PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101471
PRIOR APPLICATION NUMBER: 60/099602   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101472
PRIOR APPLICATION NUMBER: 60/099642   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101474
PRIOR APPLICATION NUMBER: 60/099741   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-09   PRIOR APPLICATION NUMBER: 60/101475
PRIOR APPLICATION NUMBER: 60/099754   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101476
PRIOR APPLICATION NUMBER: 60/099763   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101477
PRIOR APPLICATION NUMBER: 60/099792   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101479
PRIOR APPLICATION NUMBER: 60/099808   PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101738
PRIOR APPLICATION NUMBER: 60/099812   PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101741
PRIOR APPLICATION NUMBER: 60/099815   PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101743
PRIOR APPLICATION NUMBER: 60/099816   PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-10   PRIOR APPLICATION NUMBER: 60/101915
PRIOR APPLICATION NUMBER: 60/100385   PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-15   PRIOR APPLICATION NUMBER: 60/101916
PRIOR APPLICATION NUMBER: 60/100388   PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-15   PRIOR APPLICATION NUMBER: 60/102207
PRIOR APPLICATION NUMBER: 60/100390   PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-15   PRIOR APPLICATION NUMBER: 60/102240
PRIOR APPLICATION NUMBER: 60/100584   PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-15   PRIOR APPLICATION NUMBER: 60/102307
PRIOR APPLICATION NUMBER: 60/100627   PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-16   PRIOR APPLICATION NUMBER: 60/102330
PRIOR APPLICATION NUMBER: 60/100661   PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-16   PRIOR APPLICATION NUMBER: 60/102331
PRIOR APPLICATION NUMBER: 60/100662   PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-16   PRIOR APPLICATION NUMBER: 60/102484
PRIOR APPLICATION NUMBER: 60/100664   PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-16   PRIOR APPLICATION NUMBER: 60/102487
PRIOR APPLICATION NUMBER: 60/100683   PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-16   PRIOR APPLICATION NUMBER: 60/102570
PRIOR APPLICATION NUMBER: 60/100684   PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-17   PRIOR APPLICATION NUMBER: 60/102571
PRIOR APPLICATION NUMBER: 60/100710   PRIOR FILING DATE: 1998-09-30
                                             PRIOR APPLICATION NUMBER: 60/102684
                                             PRIOR FILING DATE: 1998-10-01
                                             PRIOR APPLICATION NUMBER: 60/102687
                                             PRIOR FILING DATE: 1998-10-01
                                             PRIOR APPLICATION NUMBER: 60/102965
                                             PRIOR FILING DATE: 1998-10-02
                                             PRIOR APPLICATION NUMBER: 60/103258
                                             PRIOR FILING DATE: 1998-10-06
                                             PRIOR APPLICATION NUMBER: 60/103314
                                             PRIOR FILING DATE: 1998-10-07
                                             PRIOR APPLICATION NUMBER: 60/103315
                                             PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-26

Query Match   98.1%;   Score 2297.5; DB 11; Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 61
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 63

Qy   62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy   122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   124 FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy   182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy   242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy   302 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 361
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 358

Qy   362 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy   422 AYLNWIYNVWKAEL 435
            |||||||||||||
Db   419 AYLNWIYNVWKAEL 432

RESULT 6
US-10-015-387A-275
; Sequence 275, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2830P1C54
;   CURRENT APPLICATION NUMBER: US/10/015,387A
;   CURRENT FILING DATE: 2001-12-12
;   Prior Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-015-387A-275

Query Match   98.1%;   Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 61
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 63

Qy   62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy   122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   124 FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy   182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy   242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy   302 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 361
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 358

Qy   362 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy   422 AYLNWIYNVWKAEL 435
            |||||||||||||
Db   419 AYLNWIYNVWKAEL 432

RESULT 7
US-10-063-735-112

; Sequence 112, Application US/10063735
; Publication No. US20030138882A1
GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerrisen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2830R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 112
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-735-112

Query Match   98.1%;   Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429; Conservative   0; Mismatches   0; Indels   5; Gaps   1;

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Qy    2  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL 61
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL 63

Qy   62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy  122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
           |||||||||||||||||||      |||||||||||||||||||||||||||
Db  124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy  182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy  242  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  239  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy  302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 358

Qy  362  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy  422  AYLNWIYNVWKAEL 435
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Db  419  AYLNWIYNVWKAEL 432
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RESULT 8
US-10-006-130A-275
; Sequence 275, Application US/10006130A
; Publication No. US2003014375A1
GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan l.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Hillan,Kenneth J.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-130A-275

Query Match   98.1%;   Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429; Conservative   0; Mismatches   0; Indels   0; Gaps   1;

```
Qy    2  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL 61
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL 63

Qy   62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy  122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
           |||||||||||||||||||      |||||||||||||||||||||||||||
Db  124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy  182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy  242  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  239  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy  302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 358

Qy  362  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy  422  AYLNWIYNVWKAEL 435
           |||||||||||||
Db  419  AYLNWIYNVWKAEL 432
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RESULT 9
US-10-199-672-330
; Sequence 330, Application US/10199672
; Publication No. US2003014442A1
GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-330

Query Match             98.1%;     Score 2297.5;  DB 12;  Length 432;
Best Local Similarity   98.8%;     Pred. No. 6.1e-222;
Matches   429;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps     1;

Qy          2  DPDSDQPLNSLDVKPLRKRPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4  DPDSDQPLNSLDVKPLRKRPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   63

Qy         62  CGQPLHFIPRKQLCDGELDCPLGBDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64  CGQPLHFIPRKQLCDGELDCPLGBDEEHCVKSFPBGPAVAVRLSKDRSTLQVLDSATGNW  123

Qy        122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLLDVVEITENSQELRMRNSSGPC  181
               ||||||||||||||||||||||||       ||||||||||||||||||||||||||||||
Db        124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLLDVVEITENSQELRMRNSSGPC  178

Qy        182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPMQVSIQYDKQHVCGGSIIDPHWVLTA  241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPMQVSIQYDKQHVCGGSIIDPHWVLTA  238

Qy        242  AHCFRKGHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS  301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239  AHCFRKGHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS  298

Qy        302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  358

Qy        362  GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359  GEVTEKMMCAGIPEGGVDTCQGDSGGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  418

Qy        422  AYLNWIYNVWKAEL  435
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Db        419  AYLNWIYNVWKAEL  432

RESULT 10
US-10-006-172A-275
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; Sequence 275, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
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; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01

; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
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; PRIOR APPLICATION NUMBER: 60/103315
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; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
```

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Query Match             98.1%;     Score 2297.5;  DB 12;  Length 432;
Best Local Similarity   98.8%;     Pred. No. 6.1e-222;
Matches 429;  Conservative 0;  Mismatches 0;  Indels 5;  Gaps 1;

Qy    2  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   63

Qy   62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  123

Qy  122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC  181
            ||||||||||||||||||||| ||     |||||||||||||||||||||||||||||
Db  124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC  178

Qy  182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      4  DPDSDQPINSLDVKPLRKRPIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     62  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW  123

Qy    122  FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC  181
           ||||||||||||||||||||||||||       |||||||||||||||||||||
Db    124  FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC  178

Qy    182  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179  LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  238

Qy    242  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS  301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239  AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS  298

Qy    302  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299  GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ  358

Qy    362  GEVTEKMMCAGIPBGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359  GEVTEKMMCAGIPBGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS  418

Qy    422  AYLNWIYNVWKAEL  435
           |||||||||||||
Db    419  AYLNWIYNVWKAEL  432
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RESULT 11
US-10-187-749-330
; Sequence 330, Application US/10187749
; Publication No.US2003015036A1
; GENERAL INFORMATION:
; FILE REFERENCE: P3430R1C1
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-330

  Query Match   98.1%; Score 2297.5; DB 12; Length 432;
  Best Local Similarity 98.8%; Pred. No. 6.1e-222;
  Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL   61
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(Alignment detail continued from RESULT 12 block below)

RESULT 12
US-10-194-457-330
; Sequence 330, Application US/10194457
; Publication No.US2003015037A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT: Chen,Jian
;  APPLICANT: Desnoyers,Luc
;  APPLICANT: Goddard,Audrey
;  APPLICANT: Godowski,Paul J.
;  APPLICANT: Gurney,Austin L.
;  APPLICANT: Pan,James
;  APPLICANT: Smith,Victoria
;  APPLICANT: Watanabe,Colin K.
;  APPLICANT: Wood,William I.
;  APPLICANT: Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C296
;  CURRENT APPLICATION NUMBER: US/10/194,457
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28

;   Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-330

Query Match        98.1%;    Score 2297.5;   DB 12;   Length 432;
Best Local Similarity  98.8%;   Pred. No. 6.1e-222;
Matches 429;   Conservative 0;   Mismatches 0;   Indels 5;   Gaps 1;

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Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL  61
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Db   4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL  63

Qy  62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy 122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
        |||||||||||||||||||||||     |||||||||||||||||||||||||||||||
Db 124 FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy 242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 239 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy 302 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 361
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 299 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 358

Qy 362 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 359 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy 422 AYLNWIYNVWKAEL 435
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Db 419 AYLNWIYNVWKAEL 432
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RESULT 13
US-10-184-642-330
; Sequence 330, Application US/10184642
; Publication No. US2003015763A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C194
; CURRENT APPLICATION NUMBER: US/10/184,642
; CURRENT FILING DATE: 2002-06-27
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-642-330

Query Match   98.1%;   Score 2297.5;   DB 12;   Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429;   Conservative 0;   Mismatches 0;   Indels 5;   Gaps 1;

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Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL  61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL  63

Qy  62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy 122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
        |||||||||||||||||||||||     |||||||||||||||||||||||||||||||
Db 124 FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy 242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 301
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 239 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy 302 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 361
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 299 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQ 358

Qy 362 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 359 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy 422 AYLNWIYNVWKAEL 435
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Db 419 AYLNWIYNVWKAEL 432
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RESULT 14
US-10-196-747-330
; Sequence 330, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C346
; CURRENT APPLICATION NUMBER: US/10/196,747
; CURRENT FILING DATE: 2002-07-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-747-330

Query Match   98.1%;   Score 2297.5;   DB 12;   Length 432;
Best Local Similarity 98.8%;   Pred. No. 6.1e-222;
Matches 429;   Conservative 0;   Mismatches 0;   Indels 5;   Gaps 1;

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Qy   2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL  61
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;       PRIOR APPLICATION NUMBER: 60/099598
;       PRIOR FILING DATE: 1998-09-09
;       Remaining Prior Application data removed - See File Wrapper or PALM.
;       NUMBER OF SEQ ID NOS: 477
;       SEQ ID NO 275
;       LENGTH: 432
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-10-015-392A-275

Query Match      98.1%;  Score 2297.5;  DB 12;  Length 432;
Best Local Similarity  98.8%;  Pred. No. 6.1e-222;
Matches  429;  Conservative   0;  Mismatches   0;  Indels   5;  Gaps   1;

Qy    2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFL 63

Qy   62 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW 123

Qy  122 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC 181
        |||||||||||||||||||||||     ||||||||||||||||||||||||||||||||
Db  124 FSACFDNFTEALAETACRQMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC 178

Qy  182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238

Qy  242 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS 301
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS 298

Qy  302 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 361
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQ 358

Qy  362 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 421
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359 GEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS 418

Qy  422 AYLNWIYNVWKAEL 435
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Db  419 AYLNWIYNVWKAEL 432

Search completed: December  2, 2003, 02:51:18
Job time : 325.904 secs
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    December 2, 2003, 00:14:04 ; Search time 31.7125 Seconds
                                            (without alignments)
                                        580.377 Million cell updates/sec

Title:          US-09-607-745-2
Perfect score:  2342
Sequence:       1 MDPDSDQPLNSLDVKPLRKP........VYTKVSAYLNWIYNVWKAEL 435

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:          328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_AA:*
         1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
         2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
         3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
         4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
         5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
         6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2338	99.8	435	3	US-09-008-271A-6	Sequence 6, Appli
2	2196	93.8	423	4	US-09-655-002-2	Sequence 2, Appli
3	676.5	28.9	492	4	US-09-342-749-2	Sequence 2, Appli
4	676.5	28.9	492	4	US-09-691-840-2	Sequence 2, Appli
5	655.5	28.0	454	3	US-09-518-046-2	Sequence 2, Appli
6	588.5	25.1	417	4	US-09-820-002-4	Sequence 4, Appli
7	584	24.9	455	3	US-09-261-416-2	Sequence 2, Appli
8	580	24.8	376	4	US-09-820-002-2	Sequence 2, Appli
9	574	24.5	416	2	US-09-000-846-2	Sequence 2, Appli
10	571	24.4	798	1	US-08-200-900A-2	Sequence 2, Appli
11	571	24.4	798	5	PCT-US94-00616-2	Sequence 2, Appli
12	568	24.3	418	1	US-08-508-448C-25	Sequence 25, Appl
13	568	24.3	418	4	US-09-370-838-82	Sequence 82, Appl
14	568	24.3	418	4	US-09-370-838-83	Sequence 83, Appl
15	566	24.2	418	4	US-09-370-838-62	Sequence 62, Appli
16	558.5	23.8	283	4	US-09-807-151-1	Sequence 1, Appli
17	558.5	23.8	283	4	US-09-478-957-1	Sequence 1, Appli
18	531.5	22.7	232	1	US-08-508-448C-19	Sequence 19, Appl
19	512.5	21.9	256	4	US-09-027-337-3	Sequence 3, Appli
20	512.5	21.9	256	4	US-09-644-600-3	Sequence 3, Appli
21	511	21.8	638	2	US-08-681-151-3	Sequence 3, Appli
22	507.5	21.7	255	3	US-08-944-483-67	Sequence 67, Appli
23	503.5	21.5	285	3	US-09-023-942A-26	Sequence 26, Appli
24	486	20.8	248	3	US-08-944-483-63	Sequence 63, Appli
25	483	20.6	314	4	US-09-023-942A-6	Sequence 6, Appli
26	482.5	20.6	284	4	US-09-387-375-7	Sequence 7, Appli
27	478	20.4	314	3	US-09-008-271A-3	Sequence 3, Appli
28	477	20.4	312	4	US-09-023-942A-4	Sequence 4, Appli
29	475	20.3	407	4	US-09-734-675-4	Sequence 4, Appli
30	472.5	20.2	317	4	US-09-386-629-7	Sequence 7, Appli
31	470	20.1	902	4	US-09-644-600-10	Sequence 10, Appli
32	467.5	20.0	290	4	US-09-386-653A-7	Sequence 7, Appli
33	466.5	19.9	405	4	US-09-734-675-2	Sequence 2, Appli
34	465.5	19.9	250	3	US-08-944-483-68	Sequence 68, Appli
35	463	19.8	855	3	US-09-027-337-2	Sequence 2, Appli
36	463	19.8	855	4	US-09-644-600-2	Sequence 2, Appli
37	458.5	19.6	316	4	US-09-387-375-9	Sequence 9, Appli
38	458.5	19.6	790	4	US-08-991-761A-13	Sequence 13, Appli
39	455.5	19.4	812	1	US-08-248-629A-1	Sequence 1, Appli
40	455.5	19.4	812	1	US-08-451-932-1	Sequence 1, Appli
41	455.5	19.4	812	1	US-08-452-260-1	Sequence 1, Appli
42	455.5	19.4	812	1	US-08-326-785-1	Sequence 1, Appli
43	455.5	19.4	812	2	US-08-612-788-1	Sequence 1, Appli
44	455.5	19.4	812	2	US-08-605-598B-1	Sequence 1, Appli
45	455.5	19.4	812	2	US-08-429-743-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-09-008-271A-6
; Sequence 6, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;            Hillman, Jennifer L.
;            Yue, Henry
;            Guegler, Karl J.
;            Corley, Neil C.
;            Tang, Tom Y.
;            Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Incyte Pharmaceuticals, Inc.
;    STREET: 3174 Porter Dr.
;    CITY: Palo Alto
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94304
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/008,271A
;    FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: <Unknown>
;    FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;    NAME: Mohan-Peterson, Sheela
;    REGISTRATION NUMBER: 41,201
;    REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 650-855-0555
;    TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;    LENGTH: 435 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
; IMMEDIATE SOURCE:
;    LIBRARY: COLNNOT13
;    CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-008-271A-6
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Query Match   99.8%;   Score 2338;   DB 3;   Length 435;
Best Local Similarity 99.8%;   Pred. No. 6.2e-231;
Matches 434;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 MDPDSDQPLNSLDVKPLRKRPIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF 60
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Db    1 MDPDSDQPLNSLDVKPLRKRPIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF 60

Qy   61 LCGQPLHPIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN 120
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Db   61 LCGQPLHPIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN 120

Qy  121 WFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 WFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGP 180

Qy  181 CLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVLT 240
        ||:||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db  181 CLSGSLVSLHCLACGESLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVLT 240

Qy  241 AAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTF 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTF 300

Qy  301 SGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAY 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAY 360

Qy  361 QGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKV 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 QGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKV 420

Qy  421 SAYLNWIYNVWKAEL 435
        |||||||||||||||
Db  421 SAYLNWIYNVWKAEL 435
```

RESULT 2
US-09-656-002-2

; Sequence 2, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/656,002
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-002-2

Query Match   93.8%;   Score 2196;   DB 4;   Length 423;
Best Local Similarity 97.1%;   Pred. No. 2.1e-216;
Matches 408;   Conservative 1;   Mismatches 11;   Indels 0;   Gaps 0;

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Qy   16 PLRKRPIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLC 75
        |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    4 PCANPVSPWRPSESVGIPIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLC 63

Qy   76 DGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAE 135
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 DGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAE 123

Qy  136 TACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACG 195
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 TACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACG 183

Qy  196 KSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK 255
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 KSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK 243

Qy  256 VRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLITFSGTVRPICLPFFDEE 315
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 VRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLITFSGTVRPICLPFFDEE 303

Qy  316 LTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPE 375
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  304 LTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTRCNADDAYQGEVTEKMMCAGIPE 363

Qy  376 GGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 435
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  364 GGVDTCQGDSGGPLMYQSDQWHVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 423
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RESULT 3
US-09-342-749-2

; Sequence 2, Application US/0934274749
; Patent No. 6165194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, DAvid H.F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-749-2

Query Match   28.9%;   Score 676.5;   DB 3;   Length 492;
Best Local Similarity 39.1%;   Pred. No. 1.2e-60;
Matches 150;   Conservative 57;   Mismatches 128;   Indels 49;   Gaps 13;

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Qy   75 CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA 134
        ||||: |||| :|||| :||:||||||:|||:||||:||||||||||:||||||  |||||
Db  133 CDGVSHCPGGEDENRCVRLY--GP-------NFILQYYSSQRKSWHPVCQDDWNENYG 181

Qy  135 ETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSG--------PCL 182
        ::|::|.|||  :||:|:||     :: :     :|: ::::|:|        ::|
Db  182 RAACRDMGY--KNNFYSSQ------GIVDDSGSTSFMKLNTSAGNVDIYKKLYHSDACS 232

Qy  183 SGSLVSLHCLACGKSL--KTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVL 239
        | |:||| |:|||| ||  |:||:||||| : | ||| ||:|: :||||| ||:|: ||:
Db  233 SKAVVSLRCIACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIIFPWIV 292

Qy  240 TAAHCFRKH-TDVFNWKVRAGSDKLGSF----PSLAVAKIIIEFNPMY---PKDNDIAL 291
        |||||  ::  :: ::| .:|::|::::|     :|.  :|::      :  PKDNDIAL
Db  293 TAAHCVEKPLNNPWHWTAFAGILR--QSFMFYGAGYQVEKVI---SHPNYDSKTKNNDIAL 348

Qy  292 MKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDS 351
        ||||.||||  :|:|:||| : :  ||   ||::|||  |::  :|| :|| :: ||::
Db  349 MKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEK-GKTSEVLNAAKVLLIET 407

Qy  352 TRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ-WHVGIVSWGYGCGG 410
Db  352
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Db   408  QRCNSRYVYDNLITPAMICAGFLQGNVDSCCQGDSGGPLVTSKNNIWLIGDTSWGSGCAK  467
          |||:             :  | |:|||||||||:   :||  |:|||||||||||||: |||  ||||

Qy   411  PSTPGVYTKVSAYLNWIYNVWKAE  434
          ||||:            ::||

Db   468  AYRPGVYGNVMVFTDWIYRQMRAD  491
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RESULT 4
US-09-691-840-2
; Sequence 2, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, DAvid H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-691-840-2

Query Match   28.9%;   Score 676.5;   DB 4;   Length 492;
Best Local Similarity 39.1%;   Pred. No. 1.2e-60;
Matches 150; Conservative 57; Mismatches 128; Indels 49; Gaps 13;

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Qy    75  CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA  134
          ||||||||||||||||||||||||:  | |:          | |:        |||||||||

Db   133  CDGVSHCPGGGEDENRCVRLIY--GP--------NFIIQVYSSQRKSWHPVCQDDWNENYG  181

Qy   135  ETACRQMGYSSKPTFRAVEIGPDQDLDVEITENSQELRMRNSSG------------PCL  182
          ||:|:  : |:          :|       : ::      |||   :          ||

Db   182  RAACRDMGY--KNNFYSSQ-------GIVDDSGSTSFMKLNTSAGNVDIYKKLYHSDACS  232

Qy   183  SGSLVSLHCLACGKSL--KTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVL  239
          |||||||||||:         |:|||||||||||||||||||||||||||||||||||

Db   233  SKAVVSLRCIACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIITPEWIV  292

Qy   240  TAAHCFRKH-TDVFNWKVRAGSDKLGSF----PSLAVAKIIIIEFNPMY---PKDNDIAL  291
          ||||:        ||:   :  : ||      :|   ::    |||||     ||:||||

Db   293  TAAHCVEKPLNNPWHWTRAFAGILR-QSFMFYGAGYQVEKVI---SHPNYDSKTKNNDIAL  348

Qy   292  MKLQFPLTFSGTVRPICLPFFDEBLTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDS  351
          ||||:          ::||           |||||||||||||||||||:||:  |||

Db   349  MKLQKPLTFNDLVKPVCLFNPGMMIQPEQLCWISGWGATEBK-GKTSEVLNAAKVLLIET  407

Qy   352  TRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGG  410
          | |:            |||||||:  | |:        ||:        :|||||||:|||

Db   408  QRCNSRYVYDNLITPAMICAGFLQGNVDSCCQGDSGGPLVTSKNNIWLIGDTSWGSGCAK  467

Qy   411  PSTPGVYTKVSAYLNWIYNVWKAE  434
          ||||:            ::||

Db   468  AYRPGVYGNVMVFTDWIYRQMRAD  491
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RESULT 5
US-09-518-046-2
; Sequence 2, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.

; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: protein
US-09-518-046-2

Query Match   28.0%;   Score 655.5;   DB 3;   Length 454;
Best Local Similarity 35.7%;   Pred. No. 1.5e-58;
Matches 158; Conservative 73; Mismatches 149; Indels 63; Gaps 18;

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Qy    22  IPMETFRKVGIPIIIALLSLASIIIVVLIKVILD---KY--YFLCGQPLHFIPRKQL   74
          ||||  :                 :|:|  :::|                |      |

Db    44  LPFFEVFSQSSSLGIIAL----ILALAIGLGIHFDCSGKYRCRSSFKC---IELITR---   92

Qy    75  CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA  134
          ||||:             |||||                  :    :  : | |

Db    93  CDGVSDCKDGEDEYRC---------------VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA  139

Qy   135  ETACRQMGYSS----------------KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL  182
          ||:|:  |:                   ||  |:||||||||||| |||||||||||||||:

Db   140  NVACAQLGFPSYVSSDNLRVSSLEGQFREFVSIDHLLPDDKVTALHHSVYVREG---CA  196

Qy   183  SGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA  241
          |||||||:|          | ||||||:||:||:||||:  ||   :|||||:|:||:

Db   197  SGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITA  256

Qy   242  AHCFRKHTDVF---NWKVRAGSDKL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMK  293
          |||    |        ::        :  | |:                 ::

Db   257  AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV--YHSKYKPKRLGNDIALMK  310

Qy   294  LQFPLTFSGTVRPICLPFFDEBLTPATPLWIIGWGFTKQNGGKMSDILLQASVQIDSTR  353
          ||||||||||   ||| :||||||||||||:|||||||||||||||||||  | ||:

Db   311  LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT-EDGGDASPVLNHAAVPLISNKI  369

Qy   354  CNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPS  412
          ||:          |||||||:  | |         ||:        :||||||:|:||||

Db   370  CNHRDVYGGIISPSMLCAGYLTGVDSCCQGDSGGPLVCQPERRLWKLVGATSFGIGCAEVN  429

Qy   413  TPGVYTKVSAYLNWIYNVWKAEL  435
          ||||:           :  : :|

Db   430  KPGVYTRVTSFLDWIHQMERDL  452
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RESULT 6
US-09-820-002-4
; Sequence 4, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 417

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; TYPE: PRT
; ORGANISM: HUMAN
US-09-820-002-4

Query Match            25.1%;   Score 588.5;  DB 4;  Length 417;
Best Local Similarity  31.5%;   Pred. No. 9.7e-52;
Matches  140;  Conservative  60;  Mismatches 161;  Indels  83;  Gaps  11;

Qy   19  KPRIPMETFRKVGIPIIALLSLASIIIVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE   78
Db   15  RPKVAALT--AGTLLLTAIGAASWAIVAVLLR----------------------------  45

Qy   79  LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC 138
Db   46  ------SDQE------------PLYPVQVSSADARLMVFDKTEGTWRLLCSSRSNARVAGLSC  90

Qy   139 RQMGYSSKPTFRAVEIGPDQDLDVVEITEN-------------SQELRMRNSSGPCLS   183
Db   91  EEMGF------LRAL--THSELDVRTAGANGTSGFFCVDEGRLPHTQRLLEVISPSDCPR 142

Qy   184 GSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAA 242
Db   143 GRFLAAICQDCGRRKLPVDRIVGGRDTSLGRWPWQVSLRYDGAHLCGGSLLSGDWVLTAA 202

Qy   243 HCFRKHTDVFN-WKVRAGSDKLGSFPSLAVAKIIIEFNPMYP-------KDNDIALMK   293
Db   203 HCFPERNRVLSRWRVFAGAVAQASPHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVH 262

Qy   294 LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR 353
Db   263 LSSPLPLTEYIQPVCLPAAGQALIVDGKICTVTGWGNT--QYYGQQAGVLQEARVPIISNDV 321

Qy   354 CNADDAYQGEVTEKRMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVVGIVSWGYGC  408
Db   322 CNGADFYGNQIKPKMFCAGYPEGGIDACQGDSGGPFVCEDSISRTPRWRLLCGIVSWGTGC 381

Qy   409 GGPSTPGVYTKVSAYLNWIYNVWK 432
Db   382 ALAQKPGVYTRVKVSDFREWIFQAIK 405


RESULT 7
US-09-261-416-2
; Sequence 2, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides
; OTHER INFORMATION: 144 to 1511 of Sequence 1
; Patent No. 6291663
US-09-261-416-2

Query Match            24.9%;   Score 584;  DB 3;  Length 455;
Best Local Similarity  34.2%;   Pred. No. 3.2e-51;
Matches  153;  Conservative  73;  Mismatches 150;  Indels  72;  Gaps  21;

Qy   22  IPMETFRKVGIPIIALLSLASIIIVVLIKVILD----KY---YPLCGQPLHFIPRKQL   74
Db   44  LPFFEVFSQSSSLGIIAL-----ILALAIGLGIHFDCSGKYRCRSSFKC---IELITR----  92

Qy   75  CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA 134
Db   93  CDGVSDCKDGEDEYRC---------------------VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA 139

Qy   135 ETACRQMGYSS------------------------------KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL 182
Db   140 NVACAQLGFPSYVSSDNLRVSSLBGQFREBFVSIDHLLPDDKVTALHHSVYVRBG--CA 196

Qy   183 SGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
Db   197 SGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFGYHLCGGSVITPLWIITA 256

Qy   242 AHCFRKHTDVF----NWKVRAGSDKL--GSFPSLAVAKIIIEFNPMY-PK--DNDIALMK 293
Db   257 AHCV----YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYXPKRLGNDIALMK 310

Qy   294 LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR 353
Db   311 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT-EDGGDASPVLNHAAVPLIS--- 366

Qy   354 CNADDAYQGEVTEKMM----CAGIPEG-GVDTCQGDSGGPLMYQSDQ-WHVGIVSWGYG  407
Db   367 -NKDLQPGRVRWHHLPLHALRGLPDGWRWNSCQGDSGSGGPLVCQERRLWKLVGATSFGIG 425

Qy   408 CGGPSTPGVYTKVSAYLNWIYNVWKAEL 435
Db   426 CADVNKPGVYTRVTSFLDWIHEQMERDL 453


RESULT 8
US-09-820-002-2
; Sequence 2, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 376
; TYPE: PRT
; ORGANISM: HUMAN
US-09-820-002-2

Query Match            24.8%;   Score 580;  DB 4;  Length 376;
Best Local Similarity  30.8%;   Pred. No. 6.2e-51;
Matches  132;  Conservative  57;  Mismatches 146;  Indels  94;  Gaps  9;

Qy   19  KPRIPMETFRKVGIPIIALLSLASIIIVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE   78
Db   15  RPKVAALT--AGTLLLTAIGAASWAIVAVLLR----------------------------  45

Qy   79  LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC 138
Db   46  ------SDQE------------PLYPVQVSSADARLMVFDKTEGTWRLLCSSRSNARVAGLSC  90

Qy   139 RQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACG-KS 197
Db   91  EEMGFLS------------------------------DCPRGRFLAAICQDCGRRK   116

Qy   198 LKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFN-WKV 256
Db   117 LPVDRIVGGRDTSLGRWPWQVSLRYDGAHLCGGSLLSGDWVLTAAHCFPERNRVLSRWRV 176

Qy   257 RAGSDKLGSFPSLAVAKIIIEFNPMYP-------KDNDIALMKLQQPPLTFSGTVRPIC  308
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Right column

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Db  101 SELDVRTAGANGTSGFFCVDEGGLRLAQRLLDVISVCD----------CPRGRFLTA 147

Qy  190 HCLACG-KSLKTPRVVGGEEASVDSWPMQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKH 248
        :::  |||| :::  ::  ||||| :::: |||||
Db  148 TCQDCGRRKLPVDRIVGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDWVLTAAHCFPER 207

Qy  249 TDVFN-WKVRAGSDKLGSFPSLAVAKIIIEFNPMYP-------KDNDIALMKLQFPLT 299
        ||  :                                    ||
Db  208 NRVLSRWRVFAGAVARTSPHAVQLGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLP 267

Qy  300 FSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDA 359
        :: :|: : |                          ||||||| :||
Db  268 LTEYIQPVCLPAAGQALVDGKVCTVTGWNT-QFYGQQAMVLQEARVPIISNEVCNSPDF 326

Qy  360 YQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVGIVSWGYGCGGPSTP 414
        ::  : ||| |||| ||||  |||  ::||
Db  327 YGNQIKPKMFCAGYPEGGIDACQGDSGGPFVCEDSISGTSRWRLCGIVSWGTGCALARKP 386

Qy  415 GVYTKVSAYLNWIYNVWK 432
        |||||  ::||  | ||
Db  387 GVYTKVTDFREWIFKAIK 404
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RESULT 10
US-08-200-900A-2
; Sequence 2, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
;  APPLICANT:
;   TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
;   NUMBER OF SEQUENCES: 38
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
;    STREET: 87 CambridgePark Drive
;    CITY: Cambridge
;    STATE: MA
;    COUNTRY: USA
;    ZIP: 02140
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/200,900A
;    FILING DATE: 23-FEB-1994
;    CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Meinert, Maureen C.
;    REGISTRATION NUMBER: 31,544
;    REFERENCE/DOCKET NUMBER: GI 5201-FWC
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (617) 876-1170 X8574
;    TELEFAX: (617) 876-5851
;   INFORMATION FOR SEQ ID NO: 2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 798 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-200-900A-2

  Query Match      24.4%;  Score 571;  DB 1;  Length 798;
  Best Local Similarity  35.0%;  Pred. No. 1.6e-49;
  Matches 133;  Conservative  67;  Mismatches 138;  Indels  42;  Gaps  15;

Qy   69 IPRKQLCDGELDCPLGEDEHCVKSFPEGPAVAVRLSKDRSTIQVLDSATGNWFSACFDN 128
         || : ||  |  ||                  :|: |||: |||  ||||| | |
Db  435 IPIVNLCDGFPHCKDGSDEAHCVRLF-NGTTDSSGLVQFR--IQSI-------WHVACAEN 485

Qy  129 FTEALAETACRQMGY----SSKPTFRAVEIGPDQDLDVVE----ITENSQELRMRNSSGP 180
         |: | |||  | |      ||| |||| |||  : | ||        ||||||||||||||
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Left column

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Db  177 FAGAVAQASPHGLQLGVQAVVYHGGYLPFRDPNSBENSNDIALVHLSSPLPLTEYIQPVC 236

Qy  309 LPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKM 368
        |: : :||| :                          :::|||
Db  237 LPAAGQALVDGKICTVTGWNT-QYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKM 295

Qy  369 MCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVGIVSWGYGCGGPSTPGVYTKVSAY 423
        ||||  |||  |||  ::||      : |||  | |||| ||| |||||
Db  296 FCAGYPEGGIDACQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDF 355

Qy  424 LNWIYNVWK 432
        | :|  | |
Db  356 REWIFQAIK 364

RESULT 9
US-09-000-846-2
; Sequence 2, Application US/09000846
; Patent No. 5981830
; GENERAL INFORMATION:
;  APPLICANT: WU, QINGYU
;  APPLICANT: SADLER, JASPER
;  TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH
;  TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
;  NUMBER OF SEQUENCES: 8
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;   STREET: 2200 CLARENDON BLVD. SUITE 1400
;   CITY: ARLINGTON
;   STATE: VA
;   COUNTRY: US
;   ZIP: 22201
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/000,846
;   FILING DATE: 30-DEC-1997
;   CLASSIFICATION: 800
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/866,058
;   FILING DATE: 30-MAY-1997
;  ATTORNEY/AGENT INFORMATION:
;   NAME: LEBOVITZ, RICHARD M.
;   REGISTRATION NUMBER: 37,067
;   REFERENCE/DOCKET NUMBER: BERLX 65P1
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-243-6333
;   TELEFAX: 703-243-6410
;  INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 416 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-000-846-2

  Query Match      24.5%;  Score 574;  DB 2;  Length 416;
  Best Local Similarity  30.8%;  Pred. No. 3e-50;
  Matches 135;  Conservative  62;  Mismatches 151;  Indels  90;  Gaps  10;

Qy   30 VGIPIIIALLSLASIIIVVLIKVILDKYYFLCGQPLHFIPRKQLCDGELDCPLGEDEEH 89
         ||  :  |||   ::                        : |||| |  || |
Db   22 VGTLLFLTGIGAASWAIVTILLQ--------------------SDQE- 48

Qy   90 CVKSFPEGPAVAVRLSKDRSTIQVLDSATGNWFSACFDNFTEALAETACRQMGY----- 143
         || ||  :::  ||  |||: |||  ||||| | |        |: | |||  | |
Db   49 -----PLYQVQLSPGDSRLAVFDKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAH 100

Qy  144 ---------SSKPTFRAVEIG----PDQDLDVVEITENSQELRMRNSSGPCLSGSIVSL 189
            ||| |||| |        |: |||||   :   ||||||||||
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RESULT 11
PCT-US94-00616-2
; Sequence 2, Application PC/TUS9400616
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
;   NUMBER OF SEQUENCES: 33
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US94/00616
;     FILING DATE:
;     CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 798 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US94-00616-2

Query Match           24.4%;  Score 571;  DB 5;  Length 798;
Best Local Similarity 35.0%;  Pred. No. 1.6e-49;
Matches  133;  Conservative  67;  Mismatches 138;  Indels 138;  Gaps 15;

Qy   69 IPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN 128
Db  435 IPLVNLCDGFPHCKDGSDEAHCVRLF-NGTTDSSGLVQFR--IQSI------WHVACAEN 485
Qy  129 FTEALAETACRQMGY---SSKPTFRAVEIGPDQDLDVVE---ITENSQELRMRNSSGP 180
Db  486 WTTQISDDVCQLLGLGTGNSSVPTF-STGGGPYVNLNTAPNGSLILTPSQQ------ 535
Qy  181 CLSGSLVSLHC--LACGKSLKT---PRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILD 234
Db  536 CLEDSLILLQCNYKSCGKKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQQVCGASLVS 595
Qy  235 PHWVLTAAHC-FRKHTDVFNWKVRAGSDKLGSF--PSLAVAKIIIIEFNPMY---PKDND 288
Db  596 RDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIIDQIVINPHYNKRRKNND 655
Qy  289 IALMKLQFPLTFSGTVRPICLPFFDEELITPATPLWIIGWGFTKQNGGKMSDILLQASVQV 348
Db  656 IAMMHLEMKVNYTDYIQPICLPEENQVPFPGRICSIAGWGALIYQ-GSTADVLQEADVPL 714
Qy  349 IDSTRCNADDAYQGEVTEKMCAGIPEGGVDTCQGDSGGPLMYQ-SDQWHVGIVSWGYG 407
Db  715 LSNEKCQ-QQMPEYNITENMVCAGYEAGGVDSCQGDSGGPLMCQENNRWLLAGVTSFGYQ 773
Qy  408 CGGPSTPGVYTKVSAYLNWI 427
Db  774 CALPNRPGVYARVPRFTEWI 793
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RESULT 12
US-08-508-448C-25
; Sequence 25, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
;   APPLICANT: Kazuyoshi YAMAOKA et al.
;   TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
;   TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Wenderoth, Lind & Ponack
;     STREET: 805 Fifteenth Street, N.W., #700
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: Wordperfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/508,448C
;     FILING DATE: July 28, 1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Warren M. Cheek, Jr.
;     REGISTRATION NUMBER: 33,367
;     REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-371-8850
;     TELEFAX:
;     TELEX:
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 418 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-508-448C-25

Query Match           24.3%;  Score 568;  DB 1;  Length 418;
Best Local Similarity 32.4%;  Pred. No. 1.2e-49;
Matches  138;  Conservative  79;  Mismatches 149;  Indels  60;  Gaps 14;

Qy   33 PIIIALLSLASIIIVVLIKVILDKYFLCGQPLHFIPRK--QLCDGELDCPL----- 83
Db   16 PYVVCFIVVAGVIIAVTIALLV---YFLAFDQKSYFYRSSFQLLNVEYNSQLNSPATQE 72
Qy   84 -----GEDEEHCVKSFPEG------PAVAVRLSKD----RSTLQVLDSATGNWFSACFD 127
Db   73 YRTLSGRIESLITTFKESNLRNQFIRAHVAKLRQDSGSVRADVVMKFQFTRNNNGASM- 131
Qy  128 NFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRN--SSGPCLSGS 185
Db  132 --KSRIESVLRQMLNNS---GNLEINP--STEITSLITDQAAANWLINECGAGPDLi- 180
Qy  186 LVSLHCLACGKSLKTPRVVGGBEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF 245
Db  181 -------TLSEQRILGGTEAEEGSWPWQVSLRLNNAHHCCGGSLINNMWILTAAHCF 229
Qy  246 RKHTDVFNWKVRAGSDKLGSFPSL-AVAKIIIIEFNMYPKDNDIALMLKLQFPLTFSGT 303
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Db   407 AYLDWI 412

RESULT 14
US-09-370-838-83
; Sequence 83, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-370-838-83

  Query Match   24.3%; Score 568; DB 4; Length 418;
  Best Local Similarity   32.4%; Pred. No. 1.2e-49;
  Matches 138; Conservative 79; Mismatches 149; Indels 60; Gaps 14;

Qy   33 PIIIALLSLASIIIVVLIKVILDKYFLCGQPLHFIPRK--QLCDGELDCPL------ 83
                  |:|| ||| :|||::||| ||:: : |::   ::
Db   16 PYVVCFIVAGVILAVTIALLV--YPLAFDQKSYFYRSSFQLLNVEYNSQLNSPATQE 72

Qy   84 -----GEDEEHCVKSFPEG------PAVAVRLSKD----RSTLQVLDSATGNWFSACFD 127
                     :|: :| |:| :::|
Db   73 YRTLSGRIESLITKTFKESNLRNQFIRAHVAKLRQDGSGVRADVVMKFQFTRNNNGASM- 131

Qy   128 NFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRN--SSGPCLSGS 185
                :: ||:| ::: ||| |:: ::| ::|:
Db   132 --KSRIESVLRQMLNNS----GNLEINP--STEITSLTDQAAANWLINECGAGPDLI-- 180

Qy   186 LVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF 245
                             :::||||||| ||: : |::||||:| ||||||||
Db   181 ----------TLSEQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNWILTAAHCF 229

Qy   246 RKHTDVFNWKVRAGSDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGT 303
                |: | ||:| ||| ::|| ||||:|:|: |::||
Db   230 RSNSNPRDWIATSGIST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKD 287

Qy   304 VRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGE 363
                |:|||||||||||||||||||||||| :|||:|::|::| |||||:|||||||:| |||
Db   288 IHSVCLPAATQNIPPGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGA 346

Qy   364 VTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVGIVSWGYGCGGSTPGVYTKVS 421
                |:|::|||||| ||||:||||||||||::|| |||||||||||||| ||||:|||
Db   347 ILSGMLCAGVPQGGVDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVT 406

Qy   422 AYLNWI 427
                ||:||:
Db   407 AYLDWI 412

RESULT 15
US-09-370-838-62
; Sequence 62, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh

Db   230 RSNSNPRDWIATSGIST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKD 287
                |::: ||| ::|| ::|::
Qy   304 VRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGE 363
                : ::||||||||||||||||||||| :|||:|::|::| |||||:|||||||:| |||
Db   288 IHSVCLPAATQNIPPGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGA 346

Qy   364 VTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVGIVSWGYGCGGSTPGVYTKVS 421
                |:|::|||||| ||||:||||||||||::|| |||||||||||:|
Db   347 ILSGMLCAGVPQGGVDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVT 406

Qy   422 AYLNWI 427
                ||:||:
Db   407 AYLDWI 412

RESULT 13
US-09-370-838-82
; Sequence 82, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Roadoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-370-838-82

  Query Match   24.3%; Score 568; DB 4; Length 418;
  Best Local Similarity   32.4%; Pred. No. 1.2e-49;
  Matches 138; Conservative 79; Mismatches 149; Indels 60; Gaps 14;

Qy   33 PIIIALLSLASIIIVVLIKVILDKYFLCGQPLHFIPRK--QLCDGELDCPL------ 83
                  |:|| ||| :|||::||| ||:: : |::   ::
Db   16 PYVVCFIVAGVILAVTIALLV--YPLAFDQKSYFYRSSFQLLNVEYNSQLNSPATQE 72

Qy   84 -----GEDEEHCVKSFPEG------PAVAVRLSKD----RSTLQVLDSATGNWFSACFD 127
                     :|: :| |:| :::|
Db   73 YRTLSGRIESLITKTFKESNLRNQFIRAHVAKLRQDGSGVRADVVMKFQFTRNNNGASM- 131

Qy   128 NFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRN--SSGPCLSGS 185
                :: ||:| ::: ||| |:: ::| ::|:
Db   132 --KSRIESVLRQMLNNS----GNLEINP--STEITSLTDQAAANWLINECGAGPDLI-- 180

Qy   186 LVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF 245
                             :::||||||| ||: : |::||||:| ||||||||
Db   181 ----------TLSEQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNWILTAAHCF 229

Qy   246 RKHTDVFNWKVRAGSDKLGSFPSL--AVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGT 303
                |: | ||:| ||| ::|| ||||:|:|: |::||
Db   230 RSNSNPRDWIATSGIST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKD 287

Qy   304 VRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGE 363
                |:|||||||||||||||||||||||| :|||:|::|::| |||||:|||||||:| |||
Db   288 IHSVCLPAATQNIPPGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGA 346

Qy   364 VTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVGIVSWGYGCGGSTPGVYTKVS 421
                |:|::|||||| ||||:||||||||||::|| |||||||||||||| ||||:|||
Db   347 ILSGMLCAGVPQGGVDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVT 406

Qy   422 AYLNWI 427

```
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 62
;     LENGTH: 418
;     TYPE: PRT
;     ORGANISM: Homo sapien
US-09-370-838-62
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Query Match        24.2%;     Score 566;  DB 4;   Length 418;
Best Local Similarity  32.2%;    Pred. No. 2e-49;
Matches  137;  Conservative  80;  Mismatches 149;  Indels  60;  Gaps   14;

Qy    33 PIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRK-QLCDGELDCPL------- 83
            : :||  |  |  :| ::|: |         |  :| : :
Db    16 PYVVCFIVAGVVILAVTIALLV---YFLAPDQKSYFYRSSFQLLNVEYNSQLNSPATQE 72

Qy    84 -----GEDEHCVKSFPEG------PAVAVRLSKD---RSTLQVLDSATGNWFSACFD 127
              : | :        :|:           ::::            |
Db    73 YRTLSGRIESLITKTFKESNLRNQFIRAHVAKLRQDGSSGVRADVVMKFQFTRNNNGASM- 131

Qy   128 NFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVEITENSQELRMRN--SSGPCLSGS 185
             :|||   :|          : :|:: : |           :|  |
Db   132 ---KSRIESVLRQMLNNS----GNLEINP--STEITSLTDQAAANWLINECGAGPDLI-- 180

Qy   186 LVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF 245
             : ||||  | :|||||| | : ::: | :||||||:
Db   181 --------TLSEQRILGGTEAEEGSWPWQVSLRLNNAHHCGGGSLINNMWILTAAHCF 229

Qy   246 RKHTDVFNWKVRAGSDKLGSFPSL--AVAKIIIEFNMYPKDNDIALMKLQFPLTFSGT 303
             : ::: | |:     ||||||    |:|||| ||: :|
Db   230 RSNSNPRDWIATSGIST--TFPKLRMVRNLIHNNYKSATHENDIALVRLENSVTFTKD 287

Qy   304 VRPICLPFPDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGE 363
             : ||| :| :| : :| | ||:|          ||  : :|     | : ||
Db   288 IHSVCLPAATQNIPPGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGA 346

Qy   364 VTEKWMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVS 421
             : :||||:| ||||||||||||||||:: |  |||||||||||||||:|||:| ||:
Db   347 ILSGMLCAGVPQQGGVDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVT 406

Qy   422 AYLNWI 427
            ||:||
Db   407 AYIDWI 412
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